

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 22, 2004, 20:18:17 ; Search time 127.5 Seconds
(without alignments)
99.280 Million cell updates/sec

Title: US-10-612-818-4

Perfect score: 125

Sequence: 1 RDGNPYAVCDKCLKFYISKISEY 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	125	100.0	81	2 Q80886	Q80886 human papil
2	125	100.0	84	2 Q80882	Q80882 human papil
3	125	100.0	90	2 Q80884	Q80884 human papil
4	125	100.0	90	2 Q80885	Q80885 human papil
5	125	100.0	91	2 Q80887	Q80887 human papil
6	125	100.0	99	2 Q919B2	Q919B2 human papil
7	125	100.0	103	2 Q919D6	Q919D6 human papil
8	125	100.0	130	2 Q919B4	Q919B4 human papil
9	125	100.0	130	2 Q919B8	Q919B8 human papil
10	125	100.0	130	2 Q919C0	Q919C0 human papil
11	125	100.0	130	2 Q919C2	Q919C2 human papil
12	125	100.0	130	2 Q919C8	Q919C8 human papil
13	125	100.0	130	2 Q919D0	Q919D0 human papil
14	125	100.0	138	2 Q919D2	Q919D2 human papil
15	125	100.0	143	2 Q919B6	Q919B6 human papil
16	125	100.0	143	2 Q919C4	Q919C4 human papil
17	125	100.0	151	2 Q12335	Q12335 human papil
18	125	100.0	151	2 Q12336	Q12336 human papil
19	125	100.0	151	2 Q76TS0	Q76TS0 human papil
20	125	100.0	151	2 Q77816	Q77816 human papil
21	125	100.0	151	2 Q77816	Q77816 human papil
22	125	100.0	151	2 Q77J37	Q77J37 human papil
23	125	100.0	151	2 Q77J35	Q77J35 human papil
24	125	100.0	151	2 Q80966	Q80966 human papil
25	125	100.0	151	2 Q89640	Q89640 human papil
26	125	100.0	151	2 Q89648	Q89648 human papil
27	125	100.0	151	2 Q89708	Q89708 human papil
28	125	100.0	151	2 Q89755	Q89755 human papil
29	125	100.0	151	2 Q89852	Q89852 human papil
30	125	100.0	151	2 Q89887	Q89887 human papil
31	125	100.0	151	2 Q8B564	Q8B564 human papil

32	125	100.0	151	2 Q8BB19	Q8BB19 human papil
33	125	100.0	151	2 Q8BB20	Q8BB20 human papil
34	125	100.0	151	2 Q8BB21	Q8BB21 human papil
35	125	100.0	151	2 Q8W8C3	Q8W8C3 human papil
36	125	100.0	151	2 Q9W931	Q9W931 human papil
37	125	100.0	151	2 Q9WMP2	Q9WMP2 human papil
38	125	100.0	151	2 Q9WMP4	Q9WMP4 human papil
39	125	100.0	151	2 Q9WMP5	Q9WMP5 human papil
40	125	100.0	151	1 V56 HPV16	P03126 human papil
41	125	100.0	158	2 Q71B17	Q71B17 human papil
42	125	100.0	158	2 Q8JMU8	Q8JMU8 human papil
43	125	100.0	158	2 Q9WH13	Q9WH13 human papil
44	125	100.0	158	2 Q9QDH3	Q9QDH3 human papil
45	125	100.0	158	2 Q9QDH9	Q9QDH9 human papil

ALIGNMENTS

RESULT 1

Q80886 PRELIMINARY; PRT; 81 AA.
AC Q80886;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U14515; AAB60569.2;
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 9784 MW; DD5FEDBC9F845B97 CRC64;

Query Match 100.0%; Score 125; DB 2; Length 81;
Best Local Similarity 100.0%; Pred.No. 6.3e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
Db 14 RDGNPYAVCDKCLKFYISKISEY 35

RESULT 2

Q80882 PRELIMINARY; PRT; 84 AA.
AC Q80882;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U14511; AAB60565.2;
DR GO: GO:0042025; C:host cell nucleus; IEA.

DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1 1
FT NON_TER 84 84
SQ SEQUENCE 84 AA; 10177 MW; 5AB6B896468E1CAA CRC64;

Query Match 100.0%; Score 125; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 6.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
DB 11 RDGNPYAVCDKCLKFYISKISEY 32

RESULT 3

Q80884 ID Q80884 PRELIMINARY; PRT; 90 AA.
AC Q80884;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14513; AAB60567.2; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1 1
FT NON_TER 90 90
SQ SEQUENCE 90 AA; 11021 MW; 47F42BBEFAACCC01 CRC64;

Query Match 100.0%; Score 125; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
DB 14 RDGNPYAVCDKCLKFYISKISEY 35

RESULT 4

Q80885 ID Q80885 PRELIMINARY; PRT; 90 AA.
AC Q80885;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14514; AAB60568.2; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.

FT NON_TER 1 1
FT NON_TER 90 90
SQ SEQUENCE 90 AA; 10964 MW; BC2531643ACBA76C CRC64;

Query Match 100.0%; Score 125; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
DB 14 RDGNPYAVCDKCLKFYISKISEY 35

RESULT 5

Q80887 ID Q80887 PRELIMINARY; PRT; 91 AA.
AC Q80887;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14515; AAB60570.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1 1
FT NON_TER 91 91
SQ SEQUENCE 91 AA; 11136 MW; 22FDF3EA185ACBA7 CRC64;

Query Match 100.0%; Score 125; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
DB 14 RDGNPYAVCDKCLKFYISKISEY 35

RESULT 6

Q919B2 ID Q919B2 PRELIMINARY; PRT; 99 AA.
AC Q919B2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404704; AAL01365.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1 1

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FT  NON TER      99
SQ  SEQUENCE    99 AA; 12005 MW;  C2B96025EC370E38 CRC64;

Query Match      100.0%; Score 125; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 7.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 RDGNPYAVCDKCLKFYISKISEY 22
    |||||
Db  31 RDGNPYAVCDKCLKFYISKISEY 52

RESULT 7
QY19D6 PRELIMINARY; PRT; 103 AA.
AC QY19D6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404692; AAL01342.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR NON_TER 1
FT 1
SQ SEQUENCE 103 AA; 12422 MW;  6F90CBA1F25449B CRC64;

Query Match      100.0%; Score 125; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 8e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 RDGNPYAVCDKCLKFYISKISEY 22
    |||||
Db  7 RDGNPYAVCDKCLKFYISKISEY 28

RESULT 8
QY19B4 PRELIMINARY; PRT; 130 AA.
AC QY19B4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404703; AAL01363.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR NON_TER 1
FT 1
SQ SEQUENCE 130 AA; 15792 MW;  B6C2147D227EEDDC CRC64;

Query Match      100.0%; Score 125; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 RDGNPYAVCDKCLKFYISKISEY 22
    |||||
Db  34 RDGNPYAVCDKCLKFYISKISEY 55

RESULT 9
QY19B8 PRELIMINARY; PRT; 130 AA.
AC QY19B8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404701; AAL01359.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR NON_TER 1
FT 1
SQ SEQUENCE 130 AA; 15775 MW;  92D3C07BF96B092F CRC64;

Query Match      100.0%; Score 125; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 RDGNPYAVCDKCLKFYISKISEY 22
    |||||
Db  34 RDGNPYAVCDKCLKFYISKISEY 55

RESULT 10
QY19C0 PRELIMINARY; PRT; 130 AA.
AC QY19C0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404700; AAL01357.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR NON_TER 1
FT 1
SQ SEQUENCE 130 AA; 15779 MW;  26D0147D396B0929 CRC64;

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FT  NON TER      99
SQ  SEQUENCE    99 AA; 12005 MW;  C2B96025EC370E38 CRC64;

Query Match      100.0%; Score 125; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 7.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 RDGNPYAVCDKCLKFYISKISEY 22
    |||||
Db  31 RDGNPYAVCDKCLKFYISKISEY 52

RESULT 7
QY19D6 PRELIMINARY; PRT; 103 AA.
AC QY19D6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404692; AAL01342.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR NON_TER 1
FT 1
SQ SEQUENCE 103 AA; 12422 MW;  6F90CBA1F25449B CRC64;

Query Match      100.0%; Score 125; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 8e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 RDGNPYAVCDKCLKFYISKISEY 22
    |||||
Db  7 RDGNPYAVCDKCLKFYISKISEY 28

RESULT 8
QY19B4 PRELIMINARY; PRT; 130 AA.
AC QY19B4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404703; AAL01363.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR NON_TER 1
FT 1
SQ SEQUENCE 130 AA; 15792 MW;  B6C2147D227EEDDC CRC64;

Query Match      100.0%; Score 125; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 RDGNPYAVCDKCLKFYISKISEY 22
    |||||
Db  34 RDGNPYAVCDKCLKFYISKISEY 55

RESULT 9
QY19B8 PRELIMINARY; PRT; 130 AA.
AC QY19B8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404701; AAL01359.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR NON_TER 1
FT 1
SQ SEQUENCE 130 AA; 15775 MW;  92D3C07BF96B092F CRC64;

Query Match      100.0%; Score 125; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 RDGNPYAVCDKCLKFYISKISEY 22
    |||||
Db  34 RDGNPYAVCDKCLKFYISKISEY 55

RESULT 10
QY19C0 PRELIMINARY; PRT; 130 AA.
AC QY19C0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404700; AAL01357.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR NON_TER 1
FT 1
SQ SEQUENCE 130 AA; 15779 MW;  26D0147D396B0929 CRC64;

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Query Match 100.0%; Score 125; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 1e-10; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGNPYAVCDKCLKFYISKISEY 22
 |||||
 Db 34 RDGNPYAVCDKCLKFYISKISEY 55

RESULT 11

Q919C2 ID Q919C2 PRELIMINARY; PRT; 130 AA.
 AC Q919C2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404699; AAL01355.1; --
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 125; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 1e-10; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGNPYAVCDKCLKFYISKISEY 22
 |||||
 Db 34 RDGNPYAVCDKCLKFYISKISEY 55

RESULT 12

Q919C8 ID Q919C8 PRELIMINARY; PRT; 130 AA.
 AC Q919C8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404696; AAL01345.1; --
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;

Query Match 100.0%; Score 125; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 1e-10; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGNPYAVCDKCLKFYISKISEY 22
 |||||
 Db 34 RDGNPYAVCDKCLKFYISKISEY 55

RESULT 13

Q919D0 ID Q919D0 PRELIMINARY; PRT; 130 AA.
 AC Q919D0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404695; AAL01347.1; --
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15735 MW; 9EPB30EEDCA21AF3 CRC64;

Query Match 100.0%; Score 125; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 1e-10; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGNPYAVCDKCLKFYISKISEY 22
 |||||
 Db 34 RDGNPYAVCDKCLKFYISKISEY 55

RESULT 14

Q919D2 ID Q919D2 PRELIMINARY; PRT; 138 AA.
 AC Q919D2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404694; AAL01345.1; --
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;

Query Match 100.0%; Score 125; DB 2; Length 138;

Best Local Similarity 100.0%; Pred. No. 1.1e-10; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
 Db 42 RDGNPYAVCDKCLKFYISKISEY 63

RESULT 15

Q919B6 PRELIMINARY; PRT; 143 AA.
 AC Q919B6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMEL; AF404702; AAL01361.1; -
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

Query Match 100.0%; Score 125; DB 2; Length 143;
 Best Local Similarity 100.0%; Pred. No. 1.1e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
 Db 47 RDGNPYAVCDKCLKFYISKISEY 68

Search completed: November 22, 2004, 20:31:48
 Job time : 128.5 secs

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OM protein - protein search, using sw model

Run on: November 22, 2004, 20:19:30 ; Search time 23.5 Seconds
(without alignments)
90.075 Million cell updates/sec

Title: US-10-612-818-4

Perfect score: 125
Sequence: 1 RDGNFYAVCDKCLKFYISKISEY 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	125	100.0	158	1	protein E6 - human
2	102	81.6	149	1	E6 protein - human
3	96	76.8	151	1	E6 protein - human
4	90	72.0	149	1	E6 protein - human
5	89	71.2	148	2	E6 protein - human
6	89	71.2	148	2	E6 protein - human
7	88	70.4	149	1	E6 protein - human
8	87	69.5	149	1	E6 protein - human
9	84	67.2	150	2	E6 protein - human
10	82	65.5	191	1	E6 protein - rhesu
11	79	63.2	158	1	E6 protein - human
12	77	61.6	155	1	E6 protein - human
13	77	61.6	155	1	E6 protein - human
14	76	60.8	158	1	E6 protein - human
15	74	59.2	154	2	E6 protein - human
16	72	57.6	148	2	E6 protein - human
17	72	57.6	153	2	E6 protein - human
18	72	57.6	154	2	E6 protein - human
19	72	57.6	155	2	E6 protein - human
20	71	56.8	150	1	E6 protein - human
21	71	56.8	158	1	E6 protein - human
22	65	52.0	142	2	E6 protein - human
23	65	52.0	158	2	E6 protein - human
24	62	49.6	154	2	E6 protein - human
25	59	47.2	153	1	E6 protein - human
26	58	46.4	150	1	E6 protein - human
27	54.5	43.6	1378	2	zinc finger protei
28	54.5	43.6	1571	2	zinc finger protei
29	53	42.4	150	1	E6 protein - human

30 51 40.8 159 1 S15614
31 51 40.8 159 2 S36497
32 51 40.8 407 2 B39240
33 51 40.8 446 2 F90332
34 51 40.8 1108 2 D36798
35 50.5 40.4 150 1 W6WL31
36 49 39.2 159 2 A85022
37 47 37.6 392 2 A05025
38 47 37.6 420 2 A72298
39 47 37.6 431 2 T37621
40 46.5 37.2 110 2 S38067
41 46.5 37.2 110 2 S50345
42 46.5 37.2 150 1 W6WL44
43 46 36.8 172 2 B82047
44 46 36.8 150 1 W6WL13
45 46 36.8 518 2 B86372

ALIGNMENTS

RESULT 1

W6WLHS
protein E6 - human papillomavirus type 16
C:Species: human papillomavirus type 16
C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C:Accession: A03682; F10427
R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A:Title: Human papillomavirus type 16 DNA sequence.
A:Reference number: A22355; MUID:85246220; PMID:2990099
A:Accession: A03682
A:Molecule type: DNA
A:Residues: 1-158 <SER>
A:Cross-references: UNIPROT:P03126; GB:K02718; NID:g333031; PIDN:AAA46939.1; PID:g333032
R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level
A:Reference number: Z17014; MUID:91162763; PMID:1848319
A:Accession: T10427
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-158 <KEN>
A:Cross-references: EMBL:K02718; NID:g333031; PIDN:AAA46939.1; PID:g333032
C:Genetics:
A:Gene: E6
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:37-73/Region: zinc finger CCCC motif
F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 125; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNFYAVCDKCLKFYISKISEY 22
|||||
DB 62 RDGNFYAVCDKCLKFYISKISEY 83

RESULT 2

W6WL35
E6 protein - human papillomavirus type 35
C:Species: human papillomavirus type 35
A:Note: host Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
R:Marich, J.B.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A:Title: The phylogenetic relationship and complete nucleotide sequence of human papillon
A:Reference number: A40824; MUID:92124753; PMID:1310198
A:Accession: E40824
A:Status: translation not shown

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C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match          72.0%; Score 90; DB 1; Length 149;
Best Local Similarity 72.7%; Pred. No. 1.5e-05;
Matches 16; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 RDGNPYAVCDKCLKFYSKISEY 22
         |||||:||||:|||||
Db       55 RDGNPFVCKVKCLRLSLKISEY 76

RESULT 5
A61237
E6 protein - human papillomavirus type 52
C:Species: human papillomavirus type 52
C:Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 03-May-1996
C:Accession: A61237
R:Takami, Y.; Kondoh, G.; Saito, J.; Noda, K.; Sudiro, T.M.; Sjahruzachman, A.; Warsa, U.
Int. J. Cancer 48, 516-522, 1991
A:Title: Cloning and characterization of human papillomavirus type 52 from cervical carcinoma
A:Reference number: A61237; PMID:91258022; PMID:1646174
A:Accession: A61237
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-148 <TAK>
C:Superfamily: papillomavirus E6 protein

Query Match          71.2%; Score 89; DB 2; Length 148;
Best Local Similarity 72.7%; Pred. No. 2.1e-05;
Matches 16; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      1 RDGNPYAVCDKCLKFYSKISEY 22
         |||||:||||:|||||
Db       55 RDNYPGVCMCLRFLSKISEY 76

RESULT 6
S36573
E6 protein - human papillomavirus type 52
C:Species: human papillomavirus type 52
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36573
R:Deliuss, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36573
A:Molecule type: DNA
A:Residues: 1-148 <DEL>
C:Cross-references: UNIPROT:P36814; EMBL:X74481; NID:G397038; PIDN:CAA52585.1; PID:G397038
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match          71.2%; Score 89; DB 2; Length 148;
Best Local Similarity 72.7%; Pred. No. 2.1e-05;
Matches 16; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      1 RDGNPYAVCDKCLKFYSKISEY 22
         |||||:||||:|||||
Db       55 RDNYPGVCMCLRFLSKISEY 76

RESULT 7
W6WL31
E6 protein - human papillomavirus type 31
C:Species: human papillomavirus type 31
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: A32444
R:Goldsbrough, M.D.; Disilvestre, D.; Temple, G.F.; Lorincz, A.T.
```



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Db      55 RDRSPYAACKRCVIFYSKINEY 76
      ||:|||||:|:|||||:|
RESULT 10
W6WL39
E6 protein - rhesus papillomavirus (type 1)
C/Species: rhesus papillomavirus
C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C/Accession: A38503
R/Ostrow, R.S.; LaBresh, K.V.; Faras, A.J.
Virology 181, 424-429, 1991
A/Title: Characterization of the complete RHPV 1 genomic sequence and an integration loc
A/Reference number: A38503; MUID:91135018; PMID:1847267
A/Accession: A38503
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-191 <OST>
A/Cross-references: UNIPROT:P22159; EMBL:M37717
C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; transforming protein; zinc finger
F/60-96/Region: zinc finger CCCC motif
F/133-169/Region: zinc finger CCCC motif
Query Match 65.6%; Score 82; DB 1; Length 191;
Best Local Similarity 63.6%; Pred. No. 0.00025;
Matches 14; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
Qy 1 RDGNPYAVCDKCLKFYKISYE 22
      |||||:|||||:|
Db 85 RQKPYGVCTICLRFYKIRKY 106
      |||||:|||||:|
RESULT 11
W6WL39
E6 protein - human papillomavirus type 39
C/Species: human papillomavirus type 39
A/Note: host Homo sapiens (man)
C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C/Accession: A38502
R/Volpers, C.; Strebeck, R.E.
Virology 181, 419-423, 1991
A/Title: Genome organization and nucleotide sequence of human papillomavirus type 39.
A/Reference number: A38502; MUID:91135017; PMID:1847266
A/Accession: A38502
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-158 <VOL>
A/Cross-references: UNIPROT:P24835; GB:M62849; EMBL:M38185; NID:G333245; PIDN:AAA47050.1
C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; transforming protein; zinc finger
F/32-68/Region: zinc finger CCCC motif
F/105-141/Region: zinc finger CCCC motif
Query Match 63.2%; Score 79; DB 1; Length 158;
Best Local Similarity 61.9%; Pred. No. 0.00057;
Matches 13; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
Qy 1 RDGNPYAVCDKCLKFYKISYE 21
      |||||:|||||:|
Db 57 RDGEPLAACQSCINFYAKIRE 77
      |||||:|||||:|
RESULT 12
W6WL43
E6 protein - human papillomavirus type 43
C/Species: human papillomavirus type 43
A/Note: host Homo sapiens (man)
C/Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C/Accession: A34144
R/Loerincz, A.T.; Quinn, A.P.; Goldsborough, M.D.; Schmidt, B.J.; Temple, G.F.
J. Virol. 63, 2829-2834, 1989
A/Title: Cloning and partial DNA sequencing of two new human papillomavirus types associat

```

A:Reference number: A34144; MUID:89259065; PMID:2542593

A:Accession: A34144

A:Molecule type: DNA

A:Residues: 1-155 <LOE>

A:Cross-references: UNIPROT:P19709; GB:M27022; NID:G341596; PIDN:AAA63453.1; PID:G703247

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; transforming protein; zinc finger

F:31-67/Region: zinc finger CCCC motif

F:104-140/Region: zinc finger CCCC motif

Query Match 61.6%; Score 77; DB 1; Length 155;
Best Local Similarity 59.1%; Pred. No. 0.0011;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYKISEY 22

DB 56 RDGYFAACLAQLQFHGKISQY 77

RESULT 13

W6W56

E6 protein - human papillomavirus type 56

C:Species: human papillomavirus type 56

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C:Accession: A33377; S36579

R:Loerincz, A. T.; Quinn, A. P.; Goldsborough, M. D.; McAllister, P.; Temple, G. F.

J. Gen. Virol. 70, 3099-3104, 1989

A:Title: Human papillomavirus type 56: a new virus detected in cervical cancers.

A:Reference number: A33377; MUID:90063558; PMID:2553440

A:Accession: A33377

A:Molecule type: DNA

A:Residues: 1-155 <LOE>

A:Cross-references: UNIPROT:P24836

R:Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36579

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-155

A:Cross-references: EMBL:X74483; NID:G397053; PIDN:CAA52596.1; PID:G397054

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; transforming protein; zinc finger

F:33-69/Region: zinc finger CCCC motif

F:106-142/Region: zinc finger CCCC motif

Query Match 61.6%; Score 77; DB 1; Length 155;
Best Local Similarity 63.6%; Pred. No. 0.0011;
Matches 14; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYKISEY 22

DB 58 RDGPPYAVCRVCLLFYSKRY 79

RESULT 14

W6WLP

E6 protein - human papillomavirus type ME180 (provirus)

C:Species: human papillomavirus type ME180

A:Note: host Homo sapiens (man)

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C:Accession: C40509

R:Reuter, S.; Delius, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.

J. Virol. 65, 5564-5568, 1991

A:Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma

A:Reference number: A40509; MUID:91374616; PMID:1716694.

A:Accession: C40509

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-158 <REU>

A:Cross-references: UNIPROT:P27962; GB:M73258

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger
F:32-68/Region: zinc finger CCCC motif
F:105-141/Region: zinc finger CCCC motif

Query Match 60.8%; Score 76; DB 1; Length 158;
Best Local Similarity 61.9%; Pred. No. 0.0015;
Matches 13; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYKISEY 21

DB 57 RDGVPLAACQSCIKFYAKIRE 77

RESULT 15

S36527

E6 protein - human papillomavirus type 53

C:Species: human papillomavirus type 53

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S36527

R:Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36527

A:Molecule type: DNA

A:Residues: 1-154

A:Cross-references: UNIPROT:P36815; EMBL:X74482; NID:G397046; PIDN:CAA52591.1; PID:G39704

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 59.2%; Score 74; DB 2; Length 154;
Best Local Similarity 68.4%; Pred. No. 0.0028;
Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYSKI 19

DB 59 RDGYPGVCKRCLLFYSKV 77

Search completed: November 22, 2004, 20:32:42

Job time : 24.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 22, 2004, 20:32:01 ; Search time 97.5 Seconds
(without alignments)
79.906 Million cell updates/sec

Title: US-10-612-818-4

Perfect score: 125

Sequence: 1 RDGNPYAVCDKCLKFYKISEY 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	125	100.0	22	16 US-10-612-818-4	Sequence 4, Appli
2	125	100.0	151	14 US-10-177-390-6	Sequence 6, Appli
3	125	100.0	171	16 US-10-472-724-2	Sequence 2, Appli
4	125	100.0	266	9 US-09-367-309A-1	Sequence 1, Appli
5	125	100.0	273	13 US-10-000-903-4	Sequence 4, Appli
6	125	100.0	292	13 US-10-000-903-10	Sequence 10, Appli
7	125	100.0	371	13 US-10-000-903-6	Sequence 6, Appli
8	125	100.0	390	13 US-10-000-903-14	Sequence 14, Appli
9	109	87.2	20	16 US-10-476-570-11	Sequence 11, Appli
10	71	56.8	172	16 US-10-472-724-6	Sequence 6, Appli
11	71	56.8	278	13 US-10-000-903-21	Sequence 21, Appli
12	71	56.8	383	13 US-10-000-903-23	Sequence 23, Appli
13	61	48.8	10	8 US-08-344-824-237	Sequence 237, App

14	57	45.6	9	8	US-08-344-824-346	Sequence 346, App
15	56	44.8	462	15	US-10-424-599-252512	Sequence 252512, A
16	54.5	43.6	95	15	US-10-425-114-67951	Sequence 67951, A
17	52.5	42.0	209	16	US-10-767-701-61305	Sequence 61305, A
18	52.5	42.0	315	17	US-10-425-115-281736	Sequence 281736, A
19	52.5	42.0	1082	16	US-10-437-963-167162	Sequence 167162, A
20	51	40.8	1103	17	US-10-739-930-6660	Sequence 6660, Ap
21	50	40.0	154	15	US-10-425-114-54840	Sequence 54840, A
22	50	40.0	300	15	US-10-424-599-233668	Sequence 233668, A
23	50	40.0	326	15	US-10-425-114-44352	Sequence 44352, A
24	49.5	39.6	134	15	US-10-424-599-198743	Sequence 198743, A
25	49.5	39.6	144	14	US-10-029-386-28819	Sequence 28819, A
26	49.5	39.6	313	9	US-09-864-761-43142	Sequence 43142, A
27	49.5	39.6	388	9	US-09-842-777-12	Sequence 12, Appli
28	49.5	39.6	1086	16	US-10-437-963-104962	Sequence 104962, A
29	49.5	39.6	1158	16	US-10-437-963-126051	Sequence 126051, A
30	49.5	39.6	1464	9	US-09-842-777-10	Sequence 10, Appli
31	49.5	39.6	1523	14	US-10-205-219-135	Sequence 135, App
32	49.5	39.6	1523	15	US-10-173-999-123	Sequence 123, App
33	49.5	39.6	1569	15	US-10-334-143-67	Sequence 67, Appli
34	49.5	39.6	1685	15	US-10-376-774-2691	Sequence 2691, Ap
35	49	39.2	135	17	US-10-739-930-10865	Sequence 10865, A
36	49	39.2	136	16	US-10-767-701-51604	Sequence 51604, A
37	49	39.2	136	17	US-10-425-115-353730	Sequence 353730, A
38	49	39.2	137	16	US-10-437-963-143525	Sequence 143525, A
39	49	39.2	167	15	US-10-425-114-64865	Sequence 64865, A
40	49	39.2	174	17	US-10-425-115-351731	Sequence 351731, A
41	49	39.2	451	15	US-10-424-599-246501	Sequence 246501, A
42	49	39.2	458	15	US-10-425-114-38721	Sequence 38721, A
43	49	39.2	463	15	US-10-282-122A-74636	Sequence 74636, A
44	49	39.2	467	16	US-10-437-963-163687	Sequence 163687, A
45	48.5	39.8	427	17	US-10-425-115-304190	Sequence 304190, A

ALIGNMENTS

RESULT 1

US-10-612-818-4
Sequence 4, Application US/10612818
Publication No. US20040110925A1
GENERAL INFORMATION:
APPLICANT: Impact Diagnostics
APPLICANT: Impact Diagnostics
TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomaviruses
TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papil
TITLE OF INVENTION: Associated Cancers
FILE REFERENCE: 3352-2-2
CURRENT APPLICATION NUMBER: US/10/612,818
CURRENT FILING DATE: 2003-07-01
PRIOR APPLICATION NUMBER: US 60/394,172
PRIOR FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: US 09/828,645
PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 22
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Derived from the E6 early coding region of HPV 16
US-10-612-818-4

Query Match 100.0%; Score 125; DB 16; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYKISEY 22

Db 1 RDGNPYAVCDKCLKFYKISEY 22

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RESULT 2
US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match 100.0%; Score 125; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
Db 55 RDGNPYAVCDKCLKFYISKISEY 76

RESULT 3
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match 100.0%; Score 125; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
Db 67 RDGNPYAVCDKCLKFYISKISEY 88

RESULT 4
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A

US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match 100.0%; Score 125; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
Db 55 RDGNPYAVCDKCLKFYISKISEY 76

RESULT 3
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match 100.0%; Score 125; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
Db 67 RDGNPYAVCDKCLKFYISKISEY 88

RESULT 4
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
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; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 125; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
Db 62 RDGNPYAVCDKCLKFYISKISEY 83

RESULT 5
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

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Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
Db 168 RDGNPYAVCDKCLKFYISKISEY 189

RESULT 6
US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
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; PRIOR APPLICATION NUMBER: GB 9717953.5
 ; PRIOR FILING DATE: 1997-08-22
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 292
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-10-000-903-10

Query Match 100.0%; Score 125; DB 13; Length 292;
 Best Local Similarity 100.0%; Pred. No. 2.2e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
 Db 187 RDGNPYAVCDKCLKFYISKISEY 208

RESULT 7
 US-10-000-903-6
 ; Sequence 6, Application US/10000903
 ; Publication No. US20020182221A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bruck, Claudine
 ; APPLICANT: Cabezon Silva, Teresa
 ; APPLICANT: Delisse, Anne-Marie Eva Bernande
 ; APPLICANT: Gerard, Catherine Marie Ghislaine
 ; APPLICANT: Lombardo-Bencheikh, Angela
 ; TITLE OF INVENTION: Vaccine
 ; FILE REFERENCE: B45107
 ; CURRENT APPLICATION NUMBER: US/10/000,903
 ; CURRENT FILING DATE: 2001-10-01
 ; PRIOR APPLICATION NUMBER: PCT/EP98/05285
 ; PRIOR FILING DATE: 1998-08-17
 ; PRIOR APPLICATION NUMBER: GB 9717953.5
 ; PRIOR FILING DATE: 1997-08-22
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 371
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-10-000-903-6

Query Match 100.0%; Score 125; DB 13; Length 371;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
 Db 168 RDGNPYAVCDKCLKFYISKISEY 189

RESULT 8
 US-10-000-903-14
 ; Sequence 14, Application US/10000903
 ; Publication No. US20020182221A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bruck, Claudine
 ; APPLICANT: Cabezon Silva, Teresa
 ; APPLICANT: Delisse, Anne-Marie Eva Bernande
 ; APPLICANT: Gerard, Catherine Marie Ghislaine
 ; APPLICANT: Lombardo-Bencheikh, Angela
 ; TITLE OF INVENTION: Vaccine
 ; FILE REFERENCE: B45107
 ; CURRENT APPLICATION NUMBER: US/10/000,903
 ; CURRENT FILING DATE: 2001-10-01
 ; PRIOR APPLICATION NUMBER: PCT/EP98/05285
 ; PRIOR FILING DATE: 1998-08-17
 ; PRIOR APPLICATION NUMBER: GB 9717953.5
 ; PRIOR FILING DATE: 1997-08-22
 ; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 14
 ; LENGTH: 390
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-10-000-903-14

Query Match 100.0%; Score 125; DB 13; Length 390;
 Best Local Similarity 100.0%; Pred. No. 3e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
 Db 187 RDGNPYAVCDKCLKFYISKISEY 208

RESULT 9
 US-10-476-570-11
 ; Sequence 11, Application US/10476570
 ; Publication No. US20040170644A1
 ; GENERAL INFORMATION:
 ; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
 ; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
 ; APPLICANT: MAILLIERE, Bernard
 ; APPLICANT: BOURGAULT-VILLADA, Isabelle
 ; APPLICANT: POUVELLE-MORATILLE, Sandra
 ; APPLICANT: GUILLET, Jean-Gerard
 ; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
 ; TITLE OF INVENTION: Papillomavirus proteins and uses thereof
 ; FILE REFERENCE: 45636-S071-US
 ; CURRENT APPLICATION NUMBER: US/10/476,570
 ; CURRENT FILING DATE: 2003-11-04
 ; PRIOR APPLICATION NUMBER: PCT/FR02/01533
 ; PRIOR FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: FR 01 05980
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 11
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 61-80
 ; US-10-476-570-11

Query Match 87.2%; Score 109; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.5e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKI 19
 Db 2 RDGNPYAVCDKCLKFYISKI 20

RESULT 10
 US-10-472-724-6
 ; Sequence 6, Application US/10472724
 ; Publication No. US20040171906A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cid-Arregui, Angel
 ; APPLICANT: Zur Hausen, Harald
 ; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
 ; FILE REFERENCE: 4121-154
 ; CURRENT APPLICATION NUMBER: US/10/472,724
 ; CURRENT FILING DATE: 2003-09-17
 ; PRIOR APPLICATION NUMBER: PCT/EP02/03271
 ; PRIOR FILING DATE: 2002-03-22
 ; PRIOR APPLICATION NUMBER: EP 01107271.7
 ; PRIOR FILING DATE: 2001-03-23
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 6

RESULT 14
US-08-344-824-346
; Sequence 346, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SEITE, Alessandro

APPLICANT: SIDNEY, John
TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
NUMBER OF SEQUENCES: 399
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
STREET: Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,824
FILING DATE: 23-NOV-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,634
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14137-80-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 346:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-344-824-346

Query Match 45.6%; Score 57; DB 8; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NPYAVCDKC 12
Db 1 NPYAVCDKC 9

RESULT 15
US-10-424-599-252512
Sequence 252512, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 252512
LENGTH: 462
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(462)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_70045C.1.pep

US-10-424-599-252512
Query Match 44.8%; Score 56; DB 15; Length 462;
Best Local Similarity 47.4%; Pred.No. 6.9;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
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Db 227 GKPYRVCDSCFVKLNKVAE 245
Search completed: November 22, 2004, 20:48:54
Job time : 99.5 secs

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OM protein - protein search, using sw model

Run on: November 22, 2004, 20:20:21 ; Search time 27.5 Seconds
(without alignments)
53.054 Million cell updates/sec

Title: US-10-612-818-4
Perfect score: 125
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Total number of hits satisfying chosen parameters: 478139

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5: /cgn2_6/prodata/1/iaa/6C COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	125	100.0	158	4	US-09-980-523A-2
2	125	100.0	162	1	US-08-316-239B-3
3	125	100.0	162	1	US-08-316-239B-4
4	125	100.0	172	3	US-08-860-165-14
5	125	100.0	172	3	US-09-359-382-14
6	125	100.0	266	3	US-08-860-165-10
7	125	100.0	266	3	US-09-359-382-10
8	125	100.0	266	4	US-09-367-309A-1
9	125	100.0	273	3	US-09-485-885-4
10	125	100.0	292	3	US-09-485-885-10
11	125	100.0	371	3	US-09-485-885-6
12	125	100.0	390	3	US-09-485-885-14
13	114	91.2	172	3	US-08-860-165-12
14	114	91.2	172	3	US-09-359-382-12
15	103	82.4	20	2	US-08-934-915-162
16	71	56.8	158	2	US-08-247-904B-10
17	71	56.8	158	3	US-08-767-942A-19
18	71	56.8	271	1	US-08-117-083-14
19	71	56.8	278	3	US-09-485-885-21
20	71	56.8	368	3	US-09-000-094-20
21	71	56.8	368	4	US-10-011-749-20
22	71	56.8	368	4	US-09-000-004-20
23	71	56.8	375	3	US-09-000-094-22
24	71	56.8	375	4	US-10-011-749-22
25	71	56.8	375	4	US-09-000-004-22
26	71	56.8	383	3	US-09-485-885-23
27	71	56.8	465	3	US-09-000-094-24

28	71	56.8	465	4	US-10-011-749-24	Sequence 24, Appl
29	71	56.8	465	4	US-09-000-004-24	Sequence 24, Appl
30	71	56.8	1587	3	US-09-000-094-46	Sequence 46, Appl
31	71	56.8	1587	4	US-10-011-749-46	Sequence 46, Appl
32	71	56.8	1587	4	US-09-000-004-46	Sequence 46, Appl
33	66	52.8	11	3	US-08-159-339A-1170	Sequence 1170, Ap
34	59	47.2	10	3	US-08-159-339A-561	Sequence 561, App
35	55	44.0	9	3	US-08-159-339A-74	Sequence 74, Appl
36	54	43.2	32	1	US-08-466-385-4	Sequence 4, Appl
37	54	43.2	32	3	US-08-164-768-4	Sequence 4, Appl
38	47	37.6	9	3	US-08-159-339A-229	Sequence 229, App
39	46	36.8	8	3	US-08-159-339A-1169	Sequence 1169, Ap
40	46	36.8	403	4	US-09-328-352-7791	Sequence 7791, Ap
41	45	36.0	9	3	US-08-159-339A-219	Sequence 219, App
42	45	36.0	524	4	US-03-408-020-10	Sequence 10, Appl
43	45	36.0	548	4	US-03-328-352-6605	Sequence 6605, Ap
44	44.5	35.6	135	4	US-09-513-599C-5846	Sequence 5846, Ap
45	44.5	35.6	3070	4	US-09-961-403-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WOBI AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 125; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
DB 62 RDGNPYAVCDKCLKFYISKISEY 83

RESULT 2

US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Jagtiani & Associates
STREET: 6126 Rocky Way Court
CITY: Centreville
STATE: VA
COUNTRY: USA
ZIP: 20120-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jagtiani, Ajay A.
REGISTRATION NUMBER: 35,205
REFERENCE/DOCKET NUMBER: UNNE-0001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 817-9453
TELEFAX: (703) 803-9387
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 125; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYKISEY 22
Db 62 RDGNPYAVCDKCLKFYKISEY 83

RESULT 3
US-08-316-239B-4
Sequence 4, Application US/08316239B
Patent No. 5679509
GENERAL INFORMATION:
APPLICANT: Wheeler, Colette M.
APPLICANT: Parmenter, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jagtiani & Associates
STREET: 6126 Rocky Way Court
CITY: Centreville
STATE: VA
COUNTRY: USA
ZIP: 20120-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jagtiani, Ajay A.
REGISTRATION NUMBER: 35,205
REFERENCE/DOCKET NUMBER: UNNE-0001

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 817-9453
TELEFAX: (703) 803-9387
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 125; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYKISEY 22
Db 62 RDGNPYAVCDKCLKFYKISEY 83

RESULT 4
US-08-860-165-14
Sequence 14, Application US/08860165A
Patent No. 6004557
GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 172
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match 100.0%; Score 125; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYKISEY 22
Db 131 RDGNPYAVCDKCLKFYKISEY 152

RESULT 5
US-09-359-382-14
Sequence 14, Application US/09359382
Patent No. 6306397
GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 017227/0148
CURRENT APPLICATION NUMBER: US/09/359,382
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: US 08/860,165
EARLIER FILING DATE: 1997-09-22

; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU P0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match 100.0%; Score 125; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
Db 131 RDGNPYAVCDKCLKFYISKISEY 152

RESULT 6
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA-VIRUS-ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU P0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 125; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
Db 62 RDGNPYAVCDKCLKFYISKISEY 83

RESULT 7
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868

; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU P0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 125; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
Db 62 RDGNPYAVCDKCLKFYISKISEY 83

RESULT 8
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 012227/0149
; CURRENT APPLICATION NUMBER: US/09/367309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 125; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
Db 62 RDGNPYAVCDKCLKFYISKISEY 83

RESULT 9
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4

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; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4
    Query Match      100.0%; Score 125; DB 3; Length 273;
    Best Local Similarity 100.0%; Pred. No. 2.7e-11;
    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
    |||||||||||||||||||
Db 168 RDGNPYAVCDKCLKFYISKISEY 189

RESULT 10
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10
    Query Match      100.0%; Score 125; DB 3; Length 292;
    Best Local Similarity 100.0%; Pred. No. 2.9e-11;
    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
    |||||||||||||||||||
Db 187 RDGNPYAVCDKCLKFYISKISEY 208

RESULT 11
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6
    Query Match      100.0%; Score 125; DB 3; Length 371;
    Best Local Similarity 100.0%; Pred. No. 3.7e-11;
    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
    |||||||||||||||||||
Db 168 RDGNPYAVCDKCLKFYISKISEY 189

RESULT 12
US-09-485-885-14
; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-14
    Query Match      100.0%; Score 125; DB 3; Length 390;
    Best Local Similarity 100.0%; Pred. No. 3.9e-11;
    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
    |||||||||||||||||||
Db 187 RDGNPYAVCDKCLKFYISKISEY 208

RESULT 13
US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; PRIOR APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12
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Query Match 91.2%; Score 114; DB 3; Length 172;
 Best Local Similarity 100.0%; Pred. No. 7.8e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GNPVAVCDKCLKFYKISEY 22
 |||||
 DB 2 GNPVAVCDKCLKFYKISEY 21

RESULT 14

US-09-359-382-12
 ; Sequence 12, Application US/09359382
 ; Patent No. 6306397
 ; GENERAL INFORMATION:
 ; APPLICANT: EDWARDS, Stirling John
 ; APPLICANT: COX, John Cooper
 ; APPLICANT: WEBB, Elizabeth Ann
 ; APPLICANT: FRAZER, Ian
 ; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
 ; FILE REFERENCE: 017227/0148
 ; CURRENT APPLICATION NUMBER: US/09/359,382
 ; CURRENT FILING DATE: 1999-07-23
 ; EARLIER APPLICATION NUMBER: US 08/860,165
 ; EARLIER FILING DATE: 1997-09-22
 ; EARLIER APPLICATION NUMBER: PCT/AU95/00868
 ; EARLIER FILING DATE: 1995-12-20
 ; EARLIER APPLICATION NUMBER: AU P0157/94
 ; EARLIER FILING DATE: 1994-12-20
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 12
 ; LENGTH: 172
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus type 16
 US-09-359-382-12

Query Match 91.2%; Score 114; DB 3; Length 172;
 Best Local Similarity 100.0%; Pred. No. 7.8e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GNPVAVCDKCLKFYKISEY 22
 |||||
 DB 2 GNPVAVCDKCLKFYKISEY 21

RESULT 15

US-08-934-915-162
 ; Sequence 162, Application US/08934915
 ; Patent No. 5932412
 ; GENERAL INFORMATION:
 ; APPLICANT: DILLNER, JOAKIM
 ; APPLICANT: DILLNER, LENA
 ; APPLICANT: CHENG, HWEI-MING
 ; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
 ; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
 ; TITLE OF INVENTION: 11, 16, 31, 33 AND 56,
 ; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
 ; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
 ; NUMBER OF SEQUENCES: 193
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MASON & ASSOCIATES, P.A.
 ; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
 ; CITY: CLEARWATER
 ; STATE: FLORIDA
 ; COUNTRY: U.S.A.
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: Windows 3.0
 ; SOFTWARE: Microsoft Word 6.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/934,915
 ; FILING DATE: 22-SEP-1997

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/949,836
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: LOUISE A. Foutch
 REGISTRATION NUMBER: 37,133
 REFERENCE/DOCKET NUMBER: 1946.6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 813-538-3800
 TELEFAX: 813-538-3820
 TELEX:
 INFORMATION FOR SEQ ID NO: 162:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-934-915-162

Query Match 82.4%; Score 103; DB 2; Length 20;
 Best Local Similarity 90.0%; Pred. No. 3.8e-09;
 Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYKIS 20
 |||||
 DB 1 RGNPNYAVCNKCLKFYKIS 20

Search completed: November 22, 2004, 20:33:42
 Job time : 28.5 secs

Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 22, 2004, 20:14:12 ; Search time 113.5 Seconds
(without alignments)
69.533 Million cell updates/sec

Title: US-10-612-818-4
Perfect score: 125
Sequence: 1 RDGNFVAVCDKCLKFYISKISEY 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	125	100.0	22	8	ADI34603 HPV 16 E6
2	125	100.0	151	6	AAO22640 HPV-16 pr
3	125	100.0	151	6	AAO22636 HPV prote
4	125	100.0	151	8	ADO44072 Amino aci
5	125	100.0	158	2	AAR22766 HPV E6 pe
6	125	100.0	158	3	AAY82462 Human pap
7	125	100.0	158	4	AAB98420 Human pap
8	125	100.0	158	7	ADF09515 Human pap
9	125	100.0	158	8	ADL90078 Human pap
10	125	100.0	162	2	AAW35741 Human pap
11	125	100.0	162	2	AAW35742 Human pap
12	125	100.0	171	5	AAO22922 Human pap
13	125	100.0	172	2	AAR97563 Human pap
14	125	100.0	180	7	ADF1985 Human pap
15	125	100.0	188	2	AAR63865 HPV16 E6/
16	125	100.0	243	8	AAW99369 Papilloma
17	125	100.0	248	8	ADO44060 Amino aci
18	125	100.0	248	8	ADO44066 Amino aci
19	125	100.0	263	2	AAR27725 HPV 16 E6
20	125	100.0	266	2	AAR97561 Human pap
21	125	100.0	273	2	AAY25376 HPV fusio
22	125	100.0	273	2	AAY02632 Prot.D1/3
23	125	100.0	292	2	AAY25379 HPV fusio
24	125	100.0	292	2	AAY02635 CLYTA-E6-
25	125	100.0	371	2	AAY25377 HPV fusio

26	125	100.0	371	2	AAV02633 Prot.D1/3
27	125	100.0	390	2	AAV25381 HPV fusio
28	125	100.0	390	2	AAV02637 CLYTA-E6E
29	120	96.0	151	3	AAV57808 HPV-16 E6
30	114	91.2	172	2	AAR97562 Human pap
31	113	90.4	248	8	ADO44062 Amino aci
32	113	90.4	248	8	ADO44064 Amino aci
33	113	90.4	248	8	ADO44068 Amino aci
34	113	90.4	248	8	ADO44070 Amino aci
35	109	87.2	20	6	ABP70252 Peptide d
36	102	81.6	149	2	AAR40919 HPV E6 re
37	102	81.6	149	8	ADO44077 Amino aci
38	96	76.8	16	2	AAW29586 Peptide G
39	96	76.8	17	2	AAW29585 Peptide G
40	96	76.8	19	2	AAW29583 Peptide G
41	96	76.8	21	2	AAW29572 Peptide G
42	96	76.8	32	4	AAB31109 A polyepi
43	96	76.8	32	4	AAB31017 Polyepito
44	96	76.8	151	8	ADO44080 Amino aci
45	91	72.8	15	2	AAW29587 Peptide G

ALIGNMENTS

RESULT 1
ADI34603
ID ADI34603 standard; peptide; 22 AA.
XX AC ADI34603;
XX AC
XX DT 22-APR-2004 (first entry)
XX DE HPV 16 E6 early coding region derived peptide.
XX KW HPV; E2; E6; E7; cancer; cellular abnormality.
XX OS Human papillomavirus.
XX EN WC0004005469-A2.
XX PD 15-JAN-2004.
XX PF 02-JUL-2003; 2003WO-US020887.
XX PR 02-JUL-2002; 2002US-0394172P.
XX BR 01-JUL-2003; 2003US-00612818.
XX (IMPA-) IMPACT DIAGNOSTICS INC.

Hu YX, Rosenfeld MJ;
WPI; 2004-142978/14.
New peptides from the E2, E6 or E7 proteins of human papillomavirus (HPV) 16 or 18, useful for detecting and/or diagnosing HPV-associated cellular abnormalities or cervical dysplasia or carcinoma.
Claim 4; SEQ ID NO 4; 31pp; English.
The invention relates to an isolated protein sequence or peptide from the E2, E6 or E7 early coding region of human papillomavirus (HPV) that is soluble in an aqueous medium, and characterized by a relative lack of tryptophan, methionine and cysteine residues, and a relative abundance of glycine and asparagine residues. The protein sequences can be used in a method for detecting or diagnosing cancer or cellular abnormalities. The method involves reacting a sample of body fluid or tissue likely to contain antibodies with one or more protein sequences or peptides cited above, forming an antibody-peptide complex comprising at least one of the protein sequences or peptides and the sample antibodies, and detecting the antibody-peptide complex. The protein sequences and method are useful for detecting and/or diagnosing HPV-associated epithelial cell abnormalities, precancerous conditions and cancers, such as cervical

CC cellular abnormalities selected from koilocytosis, hyperkeratosis,
 CC precancerous conditions encompassing intraepithelial lesions, high-grade
 CC dysplasias, invasive cancers and malignant cancers. The present sequence
 CC represents a specific example of a peptide derived from HPV 16 E6 early
 CC coding region.

XX Sequence 22 AA;

Query Match 100.0%; Score 125; DB 8; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.4e-12;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYKISEY 22
 DB 1 RDGNPYAVCDKCLKFYKISEY 22

RESULT 2
 AAO22640
 ID AAO22640 standard; protein; 151 AA.

XX AAO22640;
 AC AAO22640;
 XX 15-MAY-2003 (first entry)
 DT HPV-16 protein sequence, SEQ ID No 27.

DE Cytostatic; peptide therapy; immunotherapy; pre-; cancerous growth;
 KW cancer; human papilloma virus; cervix; cell-mediated immune response;
 KW HPV-16.

XX Human papilloma virus.
 OS Human papilloma virus.
 PN WO2003008649-A1.

XX 30-JAN-2003.
 PD 19-JUL-2002; 2002WO-US023198.
 PF 20-JUL-2001; 2001US-0306809P.

XX (TEXA) UNIV TEXAS SYSTEM.
 PA Sastry KJ, Tortolero-Luna G, Follen M;
 PI WPI; 2003-239363/23.

XX Determining a possible recurrence of a (pre-)cancerous growth in a
 PT patient infected with human papilloma virus (HPV), comprises incubating
 PT the sample with an HPV E6 or E7 peptide and detecting a cell-mediated
 PT immune response.

XX Disclosure; Page 129-130; 132pp; English.

XX The invention relates to a novel method for determining the possibility
 CC of recurrence of a (pre-)cancerous growth in a patient infected with
 CC human papilloma virus (HPV) or suspected of being infected with HPV, and
 CC has or had a (pre-)cancerous growth on or around the cervix. The novel
 CC method comprises incubating an E6 or E7 peptide of HPV with a sample from
 CC the patient, and assaying the sample for a cell-mediated immune response
 CC against the peptide. The method is useful for determining the possibility
 CC and preventing the recurrence of a (pre-)cancerous growth in a patient
 CC infected with HPV or suspected of being infected with HPV. The HPV E6 or
 CC E7 peptides are useful in immunotherapy for the preventing or reducing
 CC the risk of development of (pre-)cancerous growths. This sequence
 CC represents an HPV-16 protein of the invention

XX Sequence 151 AA;

Query Match 100.0%; Score 125; DB 6; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYKISEY 22
 DB 55 RDGNPYAVCDKCLKFYKISEY 76

RESULT 3

AAO22636
 ID AAO22636 standard; protein; 151 AA.

XX AAO22636;
 AC AAO22636;
 XX 15-MAY-2003 (first entry)
 DT HPV protein sequence, SEQ ID No 20.

DE Cytostatic; peptide therapy; immunotherapy; pre-; cancerous growth;
 KW cancer; human papilloma virus; cervix; cell-mediated immune response;
 KW HPV-16.

XX Human papilloma virus.
 OS Human papilloma virus.
 PN WO2003008649-A1.

XX 30-JAN-2003.
 PD 19-JUL-2002; 2002WO-US023198.
 PF 20-JUL-2001; 2001US-0306809P.

XX (TEXA) UNIV TEXAS SYSTEM.
 PA Sastry KJ, Tortolero-Luna G, Follen M;
 PI WPI; 2003-239363/23.

XX Determining a possible recurrence of a (pre-)cancerous growth in a
 PT patient infected with human papilloma virus (HPV), comprises incubating
 PT the sample with an HPV E6 or E7 peptide and detecting a cell-mediated
 PT immune response.

XX Disclosure; Page 125-126; 132pp; English.

XX The invention relates to a novel method for determining the possibility
 CC of recurrence of a (pre-)cancerous growth in a patient infected with
 CC human papilloma virus (HPV) or suspected of being infected with HPV, and
 CC has or had a (pre-)cancerous growth on or around the cervix. The novel
 CC method comprises incubating an E6 or E7 peptide of HPV with a sample from
 CC the patient, and assaying the sample for a cell-mediated immune response
 CC against the peptide. The method is useful for determining the possibility
 CC and preventing the recurrence of a (pre-)cancerous growth in a patient
 CC infected with HPV or suspected of being infected with HPV. The HPV E6 or
 CC E7 peptides are useful in immunotherapy for the preventing or reducing
 CC the risk of development of (pre-)cancerous growths. This sequence
 CC represents an HPV protein of the invention

XX Sequence 151 AA;

Query Match 100.0%; Score 125; DB 6; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYKISEY 22
 DB 55 RDGNPYAVCDKCLKFYKISEY 76

RESULT 4

ADO44072
 ID ADO44072 standard; protein; 151 AA.

XX ADO44072;
 AC ADO44072;
 XX 15-JUL-2004 (first entry)
 DT

XX DE Amino acid sequence of a wild type HPV16 E6 protein.
 XX DE
 XX DE
 KW E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
 KW cervical cancer; immune response; lower gastrointestinal tract cancer;
 KW anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
 XX
 OS Human papillomavirus type 16.
 OS Synthetic.
 OS
 PN WO2004030636-A2.
 XX
 XX 15-APR-2004.
 XX
 XX 02-OCT-2003; 2003WO-US031726.
 XX
 XX 03-OCT-2002; 2002US-0415929P.
 XX
 XX (AMHP) WYETH HOLDINGS CORP.
 XX
 XX Smith L, Cassetti MC;
 XX
 XX WPI; 2004-316328/29.
 XX
 XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
 PT useful for treating or preventing human papillomavirus (HPV)-associated
 PT cancers, e.g. cervical cancer.
 PT
 XX Claim 1; Page 76-77; 101pp; English.
 XX
 CC The present sequence represents a wild type E6 protein from human
 CC papillomavirus type 16 (HPV16), which is used to produce fusion proteins
 CC of the invention. The specification describes human papillomavirus E6 and
 CC E7 polypeptides, where the E7 polypeptide has mutations at any one or
 CC more of the amino acids corresponding to amino acids 24, 26 or 91 of the
 CC sequence given in ADO44073 and the E6 polypeptide has no mutations or has
 CC mutations at any one or more of the amino acids corresponding to amino
 CC acids 63 or 106 of there sequence given in ADO44072. The polypeptides of
 CC the invention are useful for treating or preventing human papillomavirus
 CC (HPV)-associated cancers, such as cervical cancer. The fusion proteins
 CC and nucleic acids encoding the fusion proteins are useful for generating
 CC immune responses against HPV. They are also useful for treating lower
 CC gastrointestinal tract cancers, e.g. anal cancer, and other cancers of
 CC the reproductive system, including penile and vulvar cancer.
 XX
 XX Sequence 151 AA;
 SQ
 Query Match 100.0%; Score 125; DB 8; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RDGNPYAVCDKCLFYKISEY 22
 Db 55 RDGNPYAVCDKCLFYKISEY 76
 RESULT 5
 AAR22766
 ID AAR22766 standard; peptide; 158 AA.
 XX
 AC AAR22766;
 XX
 XX 25-MAR-2003 (revised)
 DT 21-SEP-1992 (first entry)
 XX
 XX HPV E6 peptide.
 DE
 XX Human; papillomavirus; immunogenic; cervical; warts; carcinoma; cancer.
 KW
 XX Synthetic.
 OS
 OS Homo sapiens.
 XX
 XX WO9205248-A.
 PN

XX 02-APR-1992.
 PD
 XX 26-SEP-1991; 91WO-US007081.
 PF
 XX 26-SEP-1990; 90US-00588384.
 PR
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA
 XX Thomas EK, Chen L, Blake J, Hellstrom K, Hellstrom I, Hu SL;
 PI
 XX WPI; 1992-132119/16.
 DR
 XX Immunogenic peptide(s) derived from E6 or E7 region of HPV16 - and
 XX recombinant cells encoding them, useful in treatment and prophylaxis of
 PT cervical warts or cancer resulting from HPV infection.
 PT
 XX Disclosure; Fig 7; 81pp; English.
 PS
 XX The peptide is the sequence of the human papillomavirus HPV 16 E6
 CC nucleoprotein. Peptides corresponding to regions (pref. epitopic regions)
 CC of HPV 16 E6 were synthesised by standard Merrifield synthesis. Examples
 CC of such peptides are E6 1-20, 8-20, 119-134 or 148-158. Compositions
 CC contg. these peptides, antibodies against the peptides, or recombinant
 CC cells contg. the gene encoding the immuno- genic peptides may be utilised
 CC in methods for inhibiting and treating HPV infection and tumour
 CC initiation and progression e.g. in the prevention or retardation of
 CC cervical warts and cervical carcinoma resulting from HPV infection. See
 CC also AAR22767. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
 CC 25-MAR-2003 to correct PI field.)
 XX
 XX Sequence 158 AA;
 SQ
 Query Match 100.0%; Score 125; DB 2; Length 158;
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RDGNPYAVCDKCLFYKISEY 22
 Db 62 RDGNPYAVCDKCLFYKISEY 83
 RESULT 6
 AAY82462
 ID AAY82462 standard; protein; 158 AA.
 XX
 AC AAY82462;
 XX
 XX 30-JUN-2000 (first entry)
 DT
 XX Human papillomavirus E6 protein containing two zinc finger motifs.
 DE
 XX Chelated zinc finger; therapeutic; treatment; prophylaxis; MPV;
 KW mammalian papillomavirus; antiviral; cytostatic; cervical cancer; lesion;
 KW wart.
 XX
 XX Human papillomavirus.
 OS
 XX Key Location/Qualifiers
 FH
 FT Misc-difference 37..73 /note="forms a zinc finger motif"
 FT
 FT Misc-difference 110..146 /note="forms a zinc finger motif"
 FT
 XX WO200014063-A1.
 PN
 XX 16-MAR-2000.
 PD
 XX 03-SEP-1999; 99WO-AU0000724.
 XX
 XX 04-SEP-1998; 98AU-00005733.
 PR
 XX 15-JUL-1999; 99AU-00001645.
 PR
 XX

PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.
 PA (HUGH/) HUGHES E J L.
 XX Bernard H, Tan YJ, Beerheide W, Ting AE, Sim WM;
 PI WPI; 2000-356917/22.
 XX
 XX Polyulfide and dithionodisulfide agents, useful for the treatment or
 PT prophylaxis of diseases caused by mammalian papillomavirus, are
 PT disruptors of a chelated metal cation domain in an MPV gene encoded
 PT protein.
 XX
 XX Disclosure; Fig 1; 78pp; English.
 XX
 XX The present invention describes an agent used in the treatment or
 CC prophylaxis of a disease caused or exacerbated by MPV (mammalian
 CC papillomavirus) comprising a compound capable of reducing, inhibiting or
 CC otherwise decreasing the activity of a protein encoded by an MPV gene by
 CC facilitating disruption of a chelated metal cation domain present in the
 CC protein. An agent of the present invention can be used to treat cervical
 CC cancer or its HPV associated precursor lesions or other HPV associated
 CC cancers and/or warts. The present sequence represents a human
 CC papillomavirus E6 protein containing two zinc finger motifs, as given in
 CC the exemplification of the present invention
 XX
 SQ Sequence 158 AA;
 Query Match 100.0%; Score 125; DB 3; Length 158;
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RDGNPYAVCDKCLKFYKISEY 22
 DB 62 RDGNPYAVCDKCLKFYKISEY 83
 RESULT 7
 AAB98420
 ID AAB98420 standard; protein; 158 AA.
 AC AAB98420;
 XX
 XX 22-AUG-2001 (first entry)
 DT
 XX Human papillomavirus protein HPV16 E6.
 DE
 XX Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV;
 KW epitope; T cell; identification; vaccine; infection; genital wart;
 KW neoplastic growth; antiviral.
 KW
 XX Human papillomavirus.
 OS
 XX WO200141799-A1.
 PN
 XX 14-JUN-2001.
 PD
 XX 11-DEC-2000; 2000WO-US033549.
 PF
 XX 10-DEC-1999; 99US-0172705P.
 PR
 XX 15-AUG-2000; 2000US-00641528.
 XX
 XX (EPIM-) EPIMMUNE INC.
 PA
 XX Sette A, Sidney J, Southwood S, Chesnut R, Celis E, Grey HM;
 PI WPI; 2001-381497/40.
 XX
 XX An isolated human papilloma virus (HPV) epitope, useful in vaccines for
 PT treating HPV infections.
 PT
 XX Disclosure; Page 20-21; 756pp; English.
 PS
 XX The present invention describes an isolated prepared human papillomavirus

CC (HPV) epitope (I). (I) has antiviral activity, and can be used in vaccine
 CC production. Peptides and corresponding nucleic acid compositions from the
 CC present invention are useful for stimulating an immune response to HPV by
 CC stimulating the production of CII or HII responses, specifically in the
 CC treatment or prophylaxis of HPV infection, in persons who have not
 CC manifested symptoms e.g. genital warts or neoplastic growth. The peptides
 CC can also be used in a tetramer staining assay to assess peripheral blood
 CC mononuclear cells for the presence of antigen-specific CTUs following
 CC exposure to a pathogen or immunogen, and as reagents to evaluate immune
 CC recall responses or evaluate the efficacy of a vaccine. The vaccine
 CC compositions are useful for removing warts or treating HPV infections.
 CC The epitopes for inclusion in an epitope-base vaccine may be selected
 CC from conserved regions of viral or tumour-associated antigens, which
 CC reduces the likelihood of escape mutants, also immunosuppressive epitopes
 CC that may be present in whole antigens can be avoided with the use of
 CC epitope-base vaccines. An additional advantage is the ability to combine
 CC selected epitopes (CTL and HTL) and to modify the composition of the
 CC epitopes achieving enhanced immunogenicity, the major benefit of the
 CC vaccine is that is safe and efficacious. AAB98391 to AAB98477 represent
 CC polypeptide sequences used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 158 AA;
 Query Match 100.0%; Score 125; DB 4; Length 158;
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RDGNPYAVCDKCLKFYKISEY 22
 DB 62 RDGNPYAVCDKCLKFYKISEY 83
 RESULT 8
 ADF09515
 ID ADF09515 standard; protein; 158 AA.
 AC ADF09515;
 XX
 XX 12-FEB-2004 (first entry)
 DT
 XX Human papillomavirus 16 E6 SEQ ID NO:16.
 DE
 XX human; protein-protein interaction; virucide; cytostatic; vaccine;
 KW human papilloma virus; HPV; cancer.
 KW
 XX Human papillomavirus.
 OS
 XX WO2003068940-A2.
 PN
 XX 21-AUG-2003.
 PD
 XX 14-FEB-2003; 2003WO-US004594.
 PF
 XX 14-FEB-2002; 2002US-0356911P.
 PR
 XX (CURA-) CURAGEN CORP.
 PA (HOFF) HOFFMANN LA ROCHE INC.
 PA
 XX Jackson A, Ooi CE, Lewin DA, Cuthill S;
 PI WPI; 2003-689668/65.
 DR
 XX N-PSDB; ADF09607.
 DR
 XX New purified complex comprising a first polypeptide and a second
 PT polypeptide, useful for identifying agents for treating/preventing a
 PT condition involving altered level of the complex e.g. human papilloma
 PT virus infection, or cancer.
 XX
 XX Example 3; SEQ ID NO 16; 156pp; English.
 PS
 XX The invention relates to a novel purified complex comprising a first
 CC polypeptide and a second polypeptide, where the polypeptides comprise

CC defined amino acid sequences listed in the specification, and where the
 CC first polypeptide binds to the second polypeptide. A complex of the
 CC invention has virucide and cytostatic activity, and may have a use as a
 CC vaccine. The complex is useful for identifying agents for treating or
 CC preventing a conditions involving altered level of the complex, e.g.
 CC human papilloma virus (HPV) infection, or cancer. The compositions,
 CC antibodies, vectors and methods are useful for treating such diseases.
 CC The sequences shown in ADF09500-ADF09583 represent proteins of the
 CC invention.

XX SQ Sequence 158 AA;

Query Match 100.0%; Score 125; DB 7; Length 158;
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
 |||||
 Db 62 RDGNPYAVCDKCLKFYISKISEY 83

RESULT 9

ID ADL90078

XX AC ADL90078;

XX 17-JUN-2004 (first entry)

XX Human papillomavirus 16-E6 protein, SEQ ID 18.

XX Immune response; immunoglobulin; Ig; E6.

XX Human papillomavirus.

XX WO2004027049-A2.

XX 01-APR-2004.

XX 18-SEP-2003; 2003WO-US030188.

XX 20-SEP-2002; 2002US-0412219P.

XX 14-MAR-2003; 2003WO-US007995.

XX (ASTR-) ASTRAL INC.

XX Bot A, Wang L, Smith D, Phillips B;

XX WP1; 2004-295415/27.

XX Generating an immune response to an antigen, useful for generating
 PT desired T cell responses comprising administering an immunoglobulin having
 PT one peptide epitope of the antigen attached to the immunoglobulin.

XX Disclosure; Fig 1G; 154pp; English.

XX The present invention relates to a method for generating an immune
 CC response to an antigen in a patient. The method comprises administering
 CC to the patient an immunoglobulin (Ig) or its portion where the Ig has at
 CC least one peptide epitope of the antigen attached to the Ig or its
 CC portion and administering the immunoglobulin or its portion in
 CC conjunction with a RNA segment. The present sequence is an antigen
 CC sequence, used to illustrate the invention.

XX SQ Sequence 158 AA;

Query Match 100.0%; Score 125; DB 8; Length 158;
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
 |||||
 Db 62 RDGNPYAVCDKCLKFYISKISEY 83

RESULT 10

AAW35741

ID AAW35741 standard; protein; 162 AA.

XX AAW35741;

XX 25-MAR-2003 (revised)

DT 16-FEB-1998 (first entry)

XX Human papillomavirus type 16 E6 protein.

XX Complete genome; circular; human papillomavirus type 16; HPV16 E6;
 KW cervical dysplasia; cervical cancer; cervical smear.

XX Human papillomavirus type 16.

OS Location/Qualifiers

EH Misc-difference 90

FT Misc-difference 159

FT /note= "Mutated to Val in the variant"

FT /note= "End of protein sequence even though 3 amino acid
 residues are given following on"

XX US5679509-A.

XX 21-OCT-1997.

XX 30-SEP-1994; 94US-00316239.

XX 28-SEP-1993; 93US-00127906.

XX (UYNE-) UNIV NEW MEXICO STATE.

XX Wheeler CM, Parmenter CA;

XX WPI; 1997-525714/48.

XX N-PSDB; AAT94723.

XX Evaluating risk of cervical dysplasia or cervical cancer - by detecting
 PT variant form of human papilloma virus 16.

XX Claim 7; Col 23-24; 33pp; English.

XX Methods have been developed for distinguishing a subset of human
 CC papilloma virus (HPV) that is associated with an increased risk of
 CC developing cervical dysplasia or cervical cancer. The methods involve:
 CC (1) preparing a cervical sample to expose any HPV-16 E6 gene in the
 CC sample and determining if the base at position 350 of the E6 gene (see
 CC AAT94723 and AAT94724 for comparison) is T or G, where the presence of G
 CC at position 350 is associated with an increased risk of developing
 CC cervical dysplasia or cervical cancer; and (2) preparing a cervical
 CC sample to expose any HPV-16 E6 protein in the sample and determining if
 CC the amino acid at position 83 of the protein (see position 90 in AAW35741
 CC and AAW35742 for comparison) is Val or Leu, where the presence of Val at
 CC position 83 that is associated with an increased risk of developing
 CC cervical dysplasia or cervical cancer. The present sequence represents
 CC the reference protein sequence for HPV-16 E6. The 350G variant correlates
 CC well with Pap scores: 350T:350G ratios among 45 HPV16 samples were 10:4
 CC for negative Pap scores; 4:2 for CIN I, 1:6 for CIN II; 2:9 for CIN III;
 CC 0:3 for cancer. (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 162 AA;

Query Match 100.0%; Score 125; DB 2; Length 162;
 Best Local Similarity 100.0%; Pred. No. 1.4e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
 |||||
 Db 62 RDGNPYAVCDKCLKFYISKISEY 83

RESULT 11
AAW35742
ID AAW35742 standard; protein; 162 AA.
XX AC AAW35742;
XX DT 25-MAR-2003 (revised)
XX DT 16-FEB-1998 (first entry)
XX DE Human papillomavirus type 16 E6 protein variant.
XX Complete genome; circular; human papillomavirus type 16; HPV16 E6;
KW cervical dysplasia; cervical cancer; cervical smear.
XX OS Human papillomavirus type 16.
XX FH Key Location/Qualifiers
FT Misc-difference 90
FT /note= "Mutated from Leu in the reference sequence
FT (AAW35741)"
FT Misc-difference 159
FT /note= "End of protein sequence even though 3 amino acid
FT residues are given following on"
XX US5679509-A.
XX 21-OCT-1997.
XX 30-SEP-1994; 94US-00316239.
XX 28-SEP-1993; 93US-00127906.
XX (UYNF-) UNIV NEW MEXICO STATE.
XX Wheeler CM, Parmenter CA;
XX WPI; 1997-525714/48.
XX N-PSDB; AAT94742.
XX Evaluating risk of cervical dysplasia or cervical cancer - by detecting
XX variant form of human papilloma virus 16.
XX Claim 7; Col 23-26; 33pp; English.
XX Methods have been developed for distinguishing a subset of human
XX papilloma virus (HPV) that is associated with an increased risk of
XX developing cervical dysplasia or cervical cancer. The methods involve:
XX (1) preparing a cervical sample to expose any HPV-16 E6 gene in the
XX sample and determining if the base at position 350 of the E6 gene (see
XX AAT94723 and AAT94724 for comparison) is T or G, where the presence of G
XX at position 350 is associated with an increased risk of developing
XX cervical dysplasia or cervical cancer; and (2) preparing a cervical
XX sample to expose any HPV-16 E6 protein in the sample and determining if
XX the amino acid at position 83 of the protein (see position 90 in AAW35741
XX and AAW35742 for comparison) is Val or Leu, where the presence of Val at
XX position 83 that is associated with an increased risk of developing
XX cervical dysplasia or cervical cancer. The present sequence represents
XX the variant protein sequence for HPV-16 E6. The 350G variant correlates
XX well with Pap scores: 350T:350G ratios among 45 HPV16 samples were 10:4
XX for negative Pap scores; 4:2 for CIN I, 1:6 for CIN II; 2:9 for CIN III;
XX 0:3 for cancer. (Updated on 25-MAR-2003 to correct PF field.)
XX Sequence 162 AA;
Query Match 100.0%; Score 125; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RDGNPYAVCDKCLKFYISKISEY 22
DB 62 RDGNPYAVCDKCLKFYISKISEY 83

RESULT 12
AAO22922
ID AAO22922 standard; protein; 171 AA.
XX AC AAO22922;
XX DT 12-DEC-2002 (first entry)
XX DE Human papillomavirus-16 (HPV16) E6T-protein sequence.
XX Virucide; cytostatic; E6; E7 fusion protein; HPV; immunogenic; vaccine;
KW fusion partner; immunogenicity; HPV infection; neoplasm; HPV16;
KW human papillomavirus-16; E6T-sequence.
XX OS Human papillomavirus.
XX EPI243655-A1.
XX 25-SEP-2002.
XX 23-MAR-2001; 2001EP-00107271.
XX 23-MAR-2001; 2001EP-00107271.
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX Cid-Arregui A, Zur Hausen H;
XX WPI; 2002-724952/79.
XX N-PSDB; AAL53420.
XX A new DNA sequence encoding a fusion protein comprising a mutagenized HPV
XX (human papillomavirus) E6 or E7 coding sequence and a sequence encoding a
XX highly immunogenic fusion partner is useful to vaccinate against HPV
XX infection.
XX Disclosure; Fig 2; 34pp; English.
XX The invention relates to a new DNA sequence encodes an E6 or E7 fusion
XX protein of HPV, where at least 20% of the original codons are replaced by
XX codons which lead to enhanced translation in a mammalian cell, containing
XX a mutation which results in production of a truncated non-functional
XX protein, and encoding a highly immunogenic polypeptide fusion partner
XX capable of enhancing immunogenicity of the E6 or E7 protein in the
XX mammalian host. The invention is used as a vaccine for the prevention or
XX treatment of an HPV infection or a neoplasm associated with HPV
XX infection. This sequence represents the human papillomavirus-16 (HPV16)
XX E6T-protein sequence of the invention
XX Sequence 171 AA;
Query Match 100.0%; Score 125; DB 5; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RDGNPYAVCDKCLKFYISKISEY 22
DB 67 RDGNPYAVCDKCLKFYISKISEY 88
RESULT 13
AAR97563
ID AAR97563 standard; protein; 172 AA.
XX AC AAR97563;
XX DT 27-AUG-2003 (revised)
XX DT 11-JAN-1997 (first entry)
XX Human papilloma virus E6/E7 protein variant.
XX Human papilloma virus; E6; E7; deletion mutant; HPV; immune response;

KW humoral immune response; cellular immune response; vaccine.

OS Human papillomavirus.

PN WO9619496-A1.

XX 27-JUN-1996.

XX 20-DEC-1995; 95WO-AU000868.

XX 20-DEC-1994; 94AU-00000157.

XX (CSLC-) CSL LTD

XX (UYOU) UNIV QUEENSLAND.

XX Edwards SJ, Cox J, Webb EA, Frazer I;

XX WPI; 1996-309518/31.

XX N-PSDB; AAT31835.

XX Vaccine variants of human papilloma virus antigens - contain variants of E6 and/or E7 protein, pref. deletion mutants, and are used to treat or prevent HPV infection.

XX Example 3; Page 18; 37pp; English.

XX A variant of the human papilloma virus (HPV) E6 or E7 protein which elicits a humoral and/or cellular immune response against HPV can be used in vaccines against HPV or to treat HPV infection. The variant is preferably a deletion mutant comprising at least half, and preferably two-thirds of full length E6 or E7 protein starting from the N- or C-terminal, or is a full length E6 moiety fused to a full length E7 moiety. The variant optionally has a linkage moiety and a foreign protein or peptide which facilitates the purification of, and enhances the immunogenicity of, the fusion protein. This sequence is a fusion protein of the C-terminal end of E7 and the N-terminal end of E6. (Updated on 27-AUG-2003 to correct OS field.)

SQ Sequence 172 AA;

Query Match 100.0%; Score 125; DB 2; Length 172;

Best Local Similarity 100.0%; Pred. NO. 1.5e-11; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0;

QY 1 RDGNFYAVCDKCLFYKISEY 22

DB 131 RDGNFYAVCDKCLFYKISEY 152

RESULT 14

ADF31985

ID ADF31985 standard; protein; 180 AA.

AC ADF31985;

XX 12-FEB-2004 (first entry)

XX Human papillomavirus fusion gene.

XX human papillomavirus; cervix cancer.

OS Homo sapiens.

XX CN1381583-A.

XX 27-NOV-2002.

XX 24-APR-2002; 2002CN-00117143.

XX 24-APR-2002; 2002CN-00117143.

XX (ONCO-) INST ONCOLOGY TUMOR HOSPITAL CHINESE ACA.

XX

PI Zhao Q;

XX WPI; 2003-258260/26.

XX N-PSDB; ADF31984.

XX Human papillomavirus E6/E7 fusion gene and its efficient expression carrier and fusion protein vaccine.

XX Claim 8; SEQ ID NO 2; 16pp; Chinese.

XX The present invention relates to human papillomavirus E6/E7 fusion gene, its preparing process, the process for configuring the efficient expression carrier containing the gene and resultant expression carrier, the fusion protein prepared from the gene, and the application of the fusion gene and expression protein to medical science and medicine to treat cervix cancer are disclosed. The present sequence represents the human papillomavirus fusion gene.

XX Sequence 180 AA;

Query Match 100.0%; Score 125; DB 7; Length 180;

Best Local Similarity 100.0%; Pred. NO. 1.6e-11; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0;

QY 1 RDGNFYAVCDKCLFYKISEY 22

DB 62 RDGNFYAVCDKCLFYKISEY 83

RESULT 15

AAR63865

ID AAR63865 standard; protein; 188 AA.

AC AAR63865;

XX 16-OCT-2003 (revised)

XX 25-MAR-2003 (revised)

XX 28-JUN-1995 (first entry)

XX HPV16 E6/E7 proteins.

XX HPV; HPV16; E6 protein; E7 protein; diagnosis; cervical dysplasia; cervix cancer.

XX Human papillomavirus; strain 16.

XX Key Location/Qualifiers

XX Protein 1..158

XX Protein /label= E6_protein

XX Protein 159..188

XX Protein /label= E7_protein

XX WO9426934-A2.

XX 24-NOV-1994.

XX 06-MAY-1994; 94WO-US005085.

XX 06-MAY-1993; 93US-00058920.

XX (BAXT) BAXTER DIAGNOSTICS INC.

XX Brown JT;

XX WPI; 1995-006821/01.

XX P-PSDB; AAQ75470.

XX Human papilloma virus detection assay - by amplification using self sustained sequence replication and hybridisation with a detector probe.

XX Disclosure; Page 24-26; 79pp; English.

XX The sequences of the E6 and E7 polypeptide-encoding regions of human

CC papillomavirus (HPV) 16 and 18 are given in AAQ75470-71 and the encoded
 CC proteins in AAK6385-66, respectively. Probes and primers based on these
 CC sequences were used for HPV infection diagnosis; expression of E6 and E7
 CC is diagnostic for cervical cancer or pre-malignant states. (Updated on
 CC 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise
 CC OS field)

XX

SQ Sequence 188 AA;

Query Match 100.0%; Score 125; DB 2; Length 188;
 Best Local Similarity 100.0%; Pred. No. 1.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYKISEY 22
 |||||
 Db 62 RDGNPYAVCDKCLKFYKISEY 83

Search completed: November 22, 2004, 20:27:27
 Job time : 115.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 22, 2004, 20:14:12 ; Search time 113.5 Seconds
(without alignments)
69.533 Million cell updates/sec

Title: US-10-612-818-5

Perfect score: 120

Sequence: 1 KCIDFGSRIRLRHYSVSDVGD 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120	100.0	22	8	ADI34604 HPV 18 E6
2	111	92.5	32	2	AAR14751 Seroreact
3	111	92.5	158	2	AAR63866 HPV18 E6/
4	111	92.5	158	2	AAR79656 HPV-18 E6
5	111	92.5	158	2	AAY39968 HPV-18 E6
6	111	92.5	158	3	AAB03176 HPV-18 E6
7	111	92.5	158	4	AAB98427 Human pap
8	111	92.5	158	8	ADL90077 Human pap
9	111	92.5	158	8	ADO44074 Amino aci
10	111	92.5	172	5	AAR22924 Human pap
11	111	92.5	271	2	AAR2728 HPV 18 E6
12	111	92.5	278	2	AAY25385 HPV fusio
13	111	92.5	278	2	AAY02641 Prot.D1/3
14	111	92.5	383	2	AAY25386 HPV fusio
15	111	92.5	383	2	AAY02642 Prot.D1/3
16	96	80.0	158	4	AAB98440 Human pap
17	96	80.0	158	8	ADO44079 Amino aci
18	86	71.7	160	8	ADO44084 Amino aci
19	75	62.5	158	8	ADO44078 Amino aci
20	71	59.2	158	8	ADO44085 Amino aci
21	68	56.7	151	6	AAO22640 HPV-16 pr
22	68	56.7	151	6	AAO22635 HPV prote
23	68	56.7	151	8	ADO44072 Amino aci
24	68	56.7	162	2	AAR35742 Human pap
25	68	56.7	248	8	ADO44062 Amino aci

26	68	56.7	248	8	ADO44064 Amino aci
27	68	56.7	248	8	ADO44060 Amino aci
28	68	56.7	248	8	ADO44066 Amino aci
29	68	56.7	248	8	ADO44068 Amino aci
30	68	56.7	248	8	ADO44070 Amino aci
31	65	54.2	151	8	ADO44080 Amino aci
32	65	54.2	158	2	AAR22766 HPV E6 pe
33	65	54.2	158	3	AAY82462 Human pap
34	65	54.2	158	4	AAB98420 Human pap
35	65	54.2	158	7	ADF09515 Human pap
36	65	54.2	162	2	AAW35741 Human pap
37	65	54.2	171	5	AAO22922 Human pap
38	65	54.2	172	2	AAR97562 Human pap
39	65	54.2	172	2	AAR97563 Human pap
40	65	54.2	180	7	ADF31985 Human pap
41	65	54.2	188	2	AAR63865 HPV16 E6/
42	65	54.2	243	2	AAW99369 Papilloma
43	65	54.2	263	2	AAR27725 HPV 16 E6
44	65	54.2	266	2	AAR97561 Human pap
45	65	54.2	273	2	AAY25376 HPV fusio

ALIGNMENTS

RESULT 1

ADI34604

ID ADI34604 standard; peptide; 22 AA.

XX

AC ADI34604;

XX

DT 22-APR-2004 (first entry)

XX

DE HPV 18 E6 early coding region derived peptide.

XX

KW HPV; E2; E5; E7; cancer, cellular abnormality.

XX

OS Human papillomavirus.

XX

PN WO2004005469-A2.

XX

PD 15-JAN-2004.

XX

PF 02-JUL-2003; 2003WO-US020887.

XX

PR 02-JUL-2002; 2002US-0394172P.

PR

01-JUL-2003; 2003US-00612818.

XX

(IMPA-) IMPACT DIAGNOSTICS INC.

PA

Hu YX, Rosenfeld MJ;

XX

WPI; 2004-142978/14.

XX

New peptides from the E2, E6 or E7 proteins of human papillomavirus (HPV)

16 or 18, useful for detecting and/or diagnosing HPV-associated cellular

abnormalities or cervical dysplasia or carcinoma.

PT

Claim 4; SEQ ID NO 5; 31pp; English.

PS

The invention relates to an isolated protein sequence or peptide from the

E2, E6 or E7 early coding region of human papillomavirus (HPV) that is

soluble in an aqueous medium, and characterized by a relative abundance of

tryptophan, methionine and cysteine residues, and a relative abundance of

glycine and asparagine residues. The protein sequences can be used in a

method for detecting or diagnosing cancer or cellular abnormalities. The

method involves reacting a sample of body fluid or tissue likely to

contain antibodies with one or more protein sequences or peptides cited

above, forming an antibody-peptide complex comprising at lease one of the

protein sequences or peptides and the sample antibodies, and detecting

the antibody-peptide complex. The protein sequences and method are useful

for detecting and/or diagnosing HPV-associated epithelial cell

abnormalities, precancerous conditions and cancers, such as cervical

CC cellular abnormalities selected from kolloidcytosis, hyperkeratosis,
 CC precancerous conditions encompassing intraepithelial lesions, high-grade
 CC dysplasias, invasive cancers and malignant cancers. The present sequence
 CC represents a specific example of a peptide derived from HPV 18 E6 early
 CC coding region.

XX
 SQ Sequence 22 AA;

Query Match 100.0%; Score 120; DB 8; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.6e-12;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRRLRHYSVYGD 22
 |||||
 DB 1 KCIDFGSRIRRLRHYSVYGD 22

RESULT 2

AAR14751

ID AAR14751 standard; protein; 32 AA.

XX
 AC AAR14751;

XX
 DT 28-JAN-1992 (first entry)

XX Seroreactive epitope #3 of HPV 18 protein E6.

DE vaccine; HPV18.

XX Synthetic.

OS EP456197-A.

XX
 PN 13-NOV-1991.

XX
 PD 07-MAY-1991; 91EP-00107423.

XX
 PF 10-MAY-1990; 90DE-04015044.

XX
 PR (BEHW) BEHRINGWERKE AG.

XX
 PI Bleul C, Gissmann L, Muller M;

XX
 PI WPI; 1991-334182/46.

XX
 DR New sero-reactive epitope(s) of human papilloma virus 18 proteins - and

XX
 PT corresp. proteins and antibodies, useful in vaccines and for diagnosis.

XX
 PT Claim 2; Page 5; 8pp; German.

XX
 PS This peptide can be used to identify antibodies specific to E6 protein.

XX
 CC It is also useful for a vaccine against HPV18. The E6 epitope was

XX
 CC identified using anti-E6 serum to screen a recombinant phage expression

XX
 CC library containing 100bp fragments of HPV18 DNA. The DNA inserts from

XX
 CC positive phage were sequenced and based on this information, overlapping

XX
 CC decapeptides were prepared on polyethylene pins. They were tested (ELISA)

XX
 CC against the antisera to locate the epitopes. See AAR14748-R14753

XX
 SQ Sequence 32 AA;

Query Match 92.5%; Score 111; DB 2; Length 32;
 Best Local Similarity 95.5%; Pred. No. 7.7e-11;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRRLRHYSVYGD 22
 |||||
 DB 5 KCIDFYSRIRRLRHYSVYGD 26

RESULT 3

AAR63866

ID AAR63866 standard; protein; 158 AA.

XX

AC AAR63866;
 XX 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 28-JUN-1995 (first entry)
 XX
 XX HPV18 E6/E7 proteins.
 XX
 XX HPV; HPV18; E6 protein; E7 protein; diagnosis; cervical dysplasia;
 KW cervix cancer.
 XX
 XX Human papillomavirus; strain 18.
 OS
 XX WO9426934-A2.
 XX
 XX 24-NOV-1994.
 XX
 XX 06-MAY-1994; 94WO-US005085.
 XX
 XX 06-MAY-1993; 93US-00058920.
 XX
 XX (BAXT) BAXTER DIAGNOSTICS INC.
 XX
 XX Brown JT;
 XX
 XX WPI; 1995-006821/01.
 DR P-PSDB; AAQ75471.
 XX
 XX Human papilloma virus detection assay - by amplification using self
 XX sustained sequence replication and hybridisation with a detector probe.
 XX
 XX Disclosure; Page 27-28; 79pp; English.
 XX
 XX The sequences of the E6 and E7 polypeptide-encoding regions of human
 CC papillomavirus (HPV) 16 and 18 are given in AAQ75470-71 and the encoded
 CC proteins in AAR63865-66, respectively. Probes and primers based on these
 CC sequences were used for HPV infection diagnosis; expression of E6 and E7
 CC is diagnostic for cervical cancer or pre-malignant states. (Updated on
 CC 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise
 CC OS field)
 XX
 SQ Sequence 158 AA;

Query Match 92.5%; Score 111; DB 2; Length 158;
 Best Local Similarity 95.5%; Pred. No. 4.6e-10;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRRLRHYSVYGD 22
 |||||
 DB 67 KCIDFYSRIRRLRHYSVYGD 88

RESULT 4

AAR79656

ID AAR79656 standard; protein; 158 AA.

XX
 AC AAR79656;

XX
 DT 25-MAR-2003 (revised)

XX
 DT 06-DEC-1995 (first entry)

XX
 DE HPV-18 E6 protein.

XX
 KW Ubiquitin-conjugating enzyme; HPV-18 E6 protein; cell cycle;

XX
 KW cell proliferation; cancer; psoriasis; fibrosis.

XX
 OS Homo sapiens.

XX
 XX WO9518974-A2.

XX
 PD 13-JUL-1995.

XX
 XX 04-JAN-1995; 95WO-US000164.


```

XX 04-JAN-1994; 94US-00176937.
PR 23-MAY-1994; 94US-00247904.
PR 27-MAY-1994; 94US-00250795.
PR 13-SEP-1994; 94US-00305520.
XX
XX (MITO-) MITOTIX INC.
XX
XX PA Draetta G, Rolfe M, Eckstein JW, Cottarel G, Gyuris J;
PI
DR WPI; 1995-255137/33.
DR N-PSDB; AAQ97848.
XX
XX Identifying inhibitors of ubiquitin mediated proteolysis of cell cycle
PT regulatory proteins - also new ubiquitin conjugating enzymes, their
PT related nucleic acid, vectors, antibodies etc., useful for regulating
PT e.g. cell proliferation.
XX
XX Disclosure; Page 100-101; 157pp; English.
XX
XX HPV-18 E6 cDNA (given in AAQ97848) was amplified from a HeLa cell cDNA
CC library using the primers given in AAQ97846-47. The gene was subcloned
CC into a baculovirus vector for expression of recombinant E6 in Sf9 insect
CC cells for use as a component of an in vitro ubiquitin conjugating system.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 158 AA;
SQ
Query Match 92.5%; Score 111; DB 2; Length 158;
Best Local Similarity 95.5%; Pred. No. 4.6e-10;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KCIDFGSRIRRLRHYSVYGD 22
Db 67 KCIDFYSRIRRLRHYSVYGD 88
XX
RESULT 5
AAV39968
ID AAV39968 standard; protein; 158 AA.
XX
XX AAV39968;
XX
DT 15-DEC-1999 (first entry)
XX
DE HPV-18 E6 protein sequence..
XX
XX Ubiquitin conjugating enzyme; UbCE; ubiquitin-mediated proteolysis;
KW cell-cycle regulatory protein; ubiquitination inhibitor; atherosclerosis;
KW proliferative disorder; cancer; restenosis; tissue connective disorder;
KW wound healing; fibrosis disorder; rheumatoid arthritis; scleroderma;
KW insulin dependent diabetes mellitus; glomerulonephritis; cirrhosis;
KW diagnosis; therapy; E6.
XX
XX Human papillomavirus.
XX
XX US5968761-A.
XX
PD 19-OCT-1999.
XX
XX 07-JUN-1995; 95US-00486663.
XX
XX 04-JAN-1994; 94US-00176937.
PR 23-MAY-1994; 94US-00247904.
PR 27-MAY-1994; 94US-00250795.
PR 13-SEP-1994; 94US-00305520.
XX
XX (MITO-) MITOTIX INC.
XX
XX Chiu MI, Cottarel G, Berlin V, Damagnez V, Draetta G, Rolfe M;
PI
DR WPI; 1999-590402/50.
DR N-PSDB; AAZ27568.

```

```

XX Identifying ubiquitination inhibitors using novel ubiquitin conjugating
PT enzymes.
XX
XX Example 2; Col 89-92; 61pp; English.
XX
XX This sequence is the human papillomavirus E6 protein. The invention
CC relates to assays for identifying an inhibitor of ubiquitin-mediated
CC proteolysis of a cell-cycle regulatory protein comprising contacting a
CC candidate agent with an ubiquitin-conjugating system and measuring the
CC level of ubiquitination. The ubiquitin-conjugating system comprises: (a)
CC a reconstituted protein mixture including a nucleic acid which hybridizes
CC (UbCE) produced by the expression of a nucleic acid which hybridizes
CC under high stringency conditions to human UbCE, Candida albicans UbCE, or
CC Schizosaccharomyces pombe UbCE coding sequences; (b) a regulatory protein
CC ; and (c) ubiquitin. The polynucleotides are useful for identifying
CC ubiquitination inhibitors. The polynucleotides, polypeptides, antisense
CC compounds and antibodies against them may also be useful for the
CC treatment and/or diagnosis of proliferative disorders (e.g. cancer,
CC atherosclerosis, or restenosis), tissue connective disorders, controlling
CC wound healing, and disorders characterized by fibrosis (e.g. rheumatoid
CC arthritis, insulin dependent diabetes mellitus, glomerulonephritis,
CC cirrhosis, and scleroderma)
XX
XX Sequence 158 AA;
SQ
Query Match 92.5%; Score 111; DB 2; Length 158;
Best Local Similarity 95.5%; Pred. No. 4.6e-10;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KCIDFGSRIRRLRHYSVYGD 22
Db 67 KCIDFYSRIRRLRHYSVYGD 89
XX
RESULT 6
AAB03176
ID AAB03176 standard; protein; 158 AA.
XX
XX AAB03176;
XX
DT 12-SEP-2003 (revised)
DT 23-OCT-2000 (first entry)
XX
XX HPV-18 E6 protein.
XX
XX HPV-18 E6; ubiquitin mediated proteolysis; human;
KW cellular protein half life; ubiquitination inhibitor; p53; cyclin;
KW cell cycle regulator; myc deregulation; human papillomavirus;
KW HPV-18 E6 protein; cervical cancer; skin cancer; epidermal hyperplasia;
KW epidermal neoplasia; psoriasis; connective tissue disorder;
KW wound healing; cytostatic; antiproliferative; anticancer; antipsoriatic.
XX
XX Human papillomavirus; 18.
XX
XX US6068982-A.
XX
PD 30-MAY-2000.
XX
XX 17-DEC-1996; 96US-00767942.
XX
XX 04-JAN-1994; 94US-00176937.
PR 23-MAY-1994; 94US-00247904.
PR 27-MAY-1994; 94US-00250795.
PR 13-SEP-1994; 94US-00305520.
PR 07-JUN-1995; 95US-00486663.
XX
XX (MITO-) MITOTIX INC.
XX
XX Chiu MI, Cottarel G, Berlin V, Draetta G, Damagnez V, Rolfe M;
PI
DR WPI; 2000-410854/35.
DR N-PSDB; AAA61623.

```

XX Identifying an inhibitor of ubiquitin mediated proteolysis of regulatory
PT protein for treating cancers involves measuring ubiquitination levels of
PT the protein in the presence of candidate agent in an eukaryotic cell.
XX
PS Example 2; Col 97-100; 73pp; English.
XX
XX The invention relates to a method of identifying an inhibitor of
CC ubiquitin-mediated proteolysis of a cell cycle regulatory protein
CC comprising contacting an engineered eukaryotic cell with a candidate
CC agent; the eukaryotic cells is engineered to express a recombinant human,
CC Candida albicans or Schizosaccharomyces pombe ubiquitin- conjugating
CC enzyme (AAB03169-B03171), a cell cycle regulatory protein (such as p53)
CC and ubiquitin. The specification also discloses novel Candida albicans
CC and Schizosaccharomyces pombe ubiquitin-conjugating enzymes, caubCE and
CC spUBCE (AAB03170, AAB03171), and two novel human ubiquitin-conjugating
CC enzymes, hUBCE and rapUBC (AAB03169, AAB03173). The ubiquitin-mediated
CC proteolysis system is the major pathway for the selective, controlled
CC degradation of intracellular proteins in eukaryotic cells. In particular,
CC this system controls the half-lives of cellular proteins, and is
CC important in controlling the levels of proteins involved in cell cycle
CC progression. Alterations in the ubiquitination of these proteins may
CC therefore play a role in the development of cancers. For example, human
CC papillomaviruses such as HPV-18 encode a transforming protein, E6
CC (AAB03176), which combines with a cellular E6-associated protein (E6-AP;
CC AAB03177) to stimulate the ubiquitination of p53, thus targeting it for
CC degradation. The ubiquitination inhibitors identified according to the
CC method of the invention are useful for treatment of cervical cancers and
CC connective tissue disorders and for controlling the wound healing
CC process. They are also useful in treatment of hyperplastic epidermal
CC conditions such as psoriasis, neoplastic epidermal conditions, skin
CC cancers e.g., basal cell carcinomas, squamous cell carcinomas. The
CC inhibitors are useful for deregulating myc expression and rendering the
CC cells sensitive to chemotherapeutic treatment or to upset the balance of
CC transformed cells and cause apoptosis to occur. Inhibitors of ubiquitin-
CC mediated degradation of cyclins are useful as antiproliferative agents.
CC The present sequence represents HPV-18 E6 protein. (Updated on 12-SEP-
CC 2003 to standardise OS field)
XX
SQ Sequence 158 AA;

Query Match 92.5%; Score 111; DB 3; Length 158;
Best Local Similarity 95.5%; Pred. No. 4.6e-10;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRLEHYSDSVYGD 22
|||||
DB 67 KCIDFYSRIRLEHYSDSVYGD 88

RESULT 7
AAB98427
ID AAB98427 standard; protein; 158 AA.
AC AAB98427;
XX
XX 22-AUG-2001 (first entry)
XX
XX Human papillomavirus protein HPV18 E6.
DE
XX Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV;
KW epitope; T cell; identification; vaccine; infection; genital wart;
KW neoplastic growth; antiviral.
XX
XX Human papillomavirus.
OS
XX
XX WO200141799-A1.
FN
XX
XX 14-JUN-2001.
PD
XX
XX 11-DEC-2000; 2000WO-US033549.
PF
XX
XX 10-DEC-1999; 99US-0172705P.
PR

PR 15-AUG-2000; 2000US-00641528.
XX (EPIM-) EPIMUNE INC.
PA
XX Sette A, Sidney J, Southwood S, Chesnut R, Cellis E, Grey HM;
FI WPI; 2001-381497/40.
XX
XX An isolated human papilloma virus (HPV) epitope, useful in vaccines for
PT treating HPV infections.
XX
XX Disclosure; Page 22; 756pp; English.
XX
XX The present invention describes an isolated prepared human papillomavirus
CC (HPV) epitope (I). (I) has antiviral activity, and can be used in vaccine
CC production. Peptides and corresponding nucleic acid compositions from the
CC present invention are useful for stimulating an immune response to HPV by
CC stimulating the production of CTL or HTL responses, specifically in the
CC treatment or prophylaxis of HPV infection, in persons who have not
CC manifested symptoms e.g. genital warts or neoplastic growth. The peptides
CC can also be used in a tetramer staining assay to assess peripheral blood
CC mononuclear cells for the presence of antigen-specific CTLs following
CC exposure to a pathogen or immunogen, and as reagents to evaluate immune
CC recall responses or evaluate the efficacy of a vaccine. The vaccine
CC compositions are useful for removing warts or treating HPV infections.
CC The epitopes for inclusion in an epitope-base vaccine may be selected
CC from conserved regions of viral or tumour-associated antigens, which
CC reduces the likelihood of escape mutants, also immunosuppressive epitopes
CC that may be present in whole antigens can be avoided with the use of
CC selected epitopes (CTL and HTL) and to modify the composition of the
CC epitopes achieving enhanced immunogenicity, the major benefit of the
CC vaccine is that is safe and efficacious. AAB98391 to AAB98477 represent
CC polypeptide sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 158 AA;

Query Match 92.5%; Score 111; DB 4; Length 158;
Best Local Similarity 95.5%; Pred. No. 4.6e-10;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRLEHYSDSVYGD 22
|||||
DB 67 KCIDFYSRIRLEHYSDSVYGD 88

RESULT 8
ADL90077
ID ADL90077 standard; protein; 158 AA.
AC ADL90077;
XX
XX 17-JUN-2004 (first entry)
XX
XX Human papillomavirus 18-E6 protein, SEQ ID 17.
DE
XX Immune response; immunoglobulin; Ig; E6.
KW
XX Human papillomavirus.
OS
XX
XX WO2004027049-A2.
FN
XX
XX 01-APR-2004.
PD
XX
XX 18-SEP-2003; 2003WO-US030188.
PF
XX
XX 20-SEP-2002; 2002US-0412219P.
PR
XX 14-MAR-2003; 2003WO-US007995.
XX
XX (ASTR-) ASTRAL INC.
PA
XX Bot A, Wang L, Smith D, Phillips B;
PI

XX WPI; 2004-295415/27.
 XX Generating an immune response to an antigen, useful for generating
 PT desired T cell responses comprises administering an immunoglobulin having
 PT one peptide epitope of the antigen attached to the immunoglobulin.
 XX
 PS Disclosure; Fig 1G; 154pp; English.
 XX
 CC The present invention relates to a method for generating an immune
 CC response to an antigen in a patient. The method comprises administering
 CC to the patient an immunoglobulin (Ig) or its portion where the Ig has at
 CC least one peptide epitope of the antigen attached to the Ig or its
 CC portion and administering the immunoglobulin or its portion in
 CC conjunction with a RNA segment. The present sequence is an antigen
 CC sequence, used to illustrate the invention.
 XX
 SQ Sequence 158 AA;
 Query Match 92.5%; Score 111; DB 8; Length 158;
 Best Local Similarity 95.5%; Pred. No. 4.6e-10;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KCIDFGSRIRRLHYSDSVYGD 22
 DB 67 KCIDFYSRIRRLHYSDSVYGD 88
 RESULT 9
 ADO44074
 ID ADO44074 standard; protein; 158 AA.
 XX
 AC ADO44074;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Amino acid sequence of the E6 polypeptide of HPV18.
 XX
 KW E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer;
 KW cervical cancer; immune response; lower gastrointestinal tract cancer;
 KW anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
 XX
 OS Human papillomavirus type 18.
 XX
 PN WO2004030636-A2.
 XX
 PD 15-APR-2004.
 XX
 PF 02-OCT-2003; 2003WO-US031726.
 XX
 PR 03-OCT-2002; 2002US-0415929P.
 XX
 PA (AMHP) WYETH HOLDINGS CORP.
 XX
 PI Smith L, Cassetti MC;
 XX
 DR WPI; 2004-316328/29.
 DR N-PSDB; ADO44101.
 XX
 CC New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
 PT useful for treating or preventing human papillomavirus (HPV)-associated
 PT cancers, e.g. cervical cancer.
 XX
 PS Disclosure; Page 78; 101pp; English.
 XX
 CC ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses.
 CC ADO44098 is the consensus sequence derived from these polypeptides. The
 CC specification describes human papillomavirus E6 and E7 polypeptides,
 CC where the E7 polypeptide has mutations at any one or more of the amino
 CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
 CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
 CC one or more of the amino acids corresponding to amino acids 63 or 106 of
 CC there sequence given in ADO44072. The polypeptides of the invention are

CC useful for treating or preventing human papillomavirus (HPV)-associated
 CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
 CC encoding the fusion proteins are useful for generating immune responses
 CC against HPV. They are also useful for treating lower gastrointestinal
 CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
 CC system, including penile and vulvar cancer.
 XX
 SQ Sequence 158 AA;
 Query Match 92.5%; Score 111; DB 8; Length 158;
 Best Local Similarity 95.5%; Pred. No. 4.6e-10;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KCIDFGSRIRRLHYSDSVYGD 22
 DB 67 KCIDFYSRIRRLHYSDSVYGD 88
 RESULT 10
 AAO22924
 ID AAO22924 standard; protein; 172 AA.
 XX
 AC AAO22924;
 XX
 DT 12-DEC-2002 (first entry)
 XX
 DE Human papillomavirus-18 (HPV18) E6E7-protein sequence.
 XX
 KW Virucide; cytostatic; E6; E7 fusion protein; HPV; immunogenic; vaccine;
 KW fusion partner; immunogenicity; HPV infection; neoplasm; HPV18;
 KW human papillomavirus-18; E6E7-sequence.
 XX
 OS Human papillomavirus.
 XX
 PN EP1243655-A1.
 XX
 PD 25-SEP-2002.
 XX
 PF 23-MAR-2001; 2001EP-00107271.
 XX
 PR 23-MAR-2001; 2001EP-00107271.
 XX
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX
 PI Cid-Arregui A, Zur Hausen H;
 XX
 DR WPI; 2002-724952/79.
 DR N-PSDB; AAL53422.
 XX
 PT A new DNA sequence encoding a fusion protein comprising a mutagenized HPV
 PT (human papillomavirus) E6 or E7 coding sequence and a sequence encoding a
 PT highly immunogenic fusion partner is useful to vaccinate against HPV
 PT infection.
 XX
 PS Disclosure; Fig 4; 34pp; English.
 XX
 CC The invention relates to a new DNA sequence encodes an E6 or E7 fusion
 CC protein of HPV, where at least 20% of the original codons are replaced by
 CC codons which lead to enhanced translation in a mammalian cell, containing
 CC a mutation which results in production of a truncated non-functional
 CC protein, and encoding a highly immunogenic polypeptide fusion partner
 CC capable of enhancing immunogenicity of the E6 or E7 protein in the
 CC mammalian host. The invention is used as a vaccine for the prevention or
 CC treatment of an HPV infection or a neoplasm associated with HPV
 CC infection. This sequence represents the human papillomavirus-18 (HPV18)
 CC E6E7-protein sequence of the invention
 XX
 SQ Sequence 172 AA;
 Query Match 92.5%; Score 111; DB 5; Length 172;
 Best Local Similarity 95.5%; Pred. No. 5.1e-10;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRRLRHYSVYGD 22
 |||||
 Db 73 KCIDFYSRIRRLRHYSVYGD 94

RESULT 11

AAAR27728
 ID AAR27728 standard; protein; 271 AA.

XX AC AAR27728;

XX DT 24-OCT-2003 (revised)

XX DT 25-MAR-2003 (revised)

XX DT 09-MAR-1993 (first entry)

XX XX HPV 18 E6 protein fragment.

XX XX Virus vector; vaccinia virus; papillomavirus; HPV; human; amplification;

XX KW immunotherapeutic.

XX XX Human papillomavirus; 18.

XX FH Key Location/Qualifiers

XX FT Peptide 2..259

XX FT /note= "HPV-18 E6 protein"

XX XX WO9216636-A1.

XX XX 01-OCT-1992.

XX XX 10-MAR-1992; 92WO-GB000424.

XX XX 14-MAR-1991; 91GB-00005383.

XX XX (IMMU) IMMUNOLOGY LTD.

XX PI Boursnell MEG, Inglis SC, Munro AJ;

XX DR WPI; 1992-349219/42.

XX DR N-PSDB; AAQ29390.

XX XX Recombinant virus vectors encoding human papillomavirus proteins - for
 PT treating and vaccinating against HPV infections and conditions caused by
 PT them, such as cervical cancer.
 XX Disclosure; Fig 1b; 83pp; English.

XX CC The fragment of DNA contg. the HPV-18 E6/E7 coding region was prepd. by
 CC PCR from plasmid pBR322/HPV16 (Boshart et al., EMBO J. 3: 1151) using
 CC oligonucleotides S01 and S02. The prod. of the second reading frame is
 CC the HPV-18 E7 protein whereas the third reading frame encodes HPV-18 E6.
 CC The E6 and E7 ORFs are fused together to form a single continuous ORF via
 CC site directed mutagenesis and the immortalising potential of E7 is
 CC removed by altering two key codons of the HPV E7 sequence. The single ORF
 CC of HPV-18 E6/E7 may be inserted into vaccinia virus DNA at neutral sites
 CC (pref. by inserting two sets of the DNA in opposite orientations to
 CC overcome the problem of intertypic recombination) to make a recombinant
 CC virus vector for use immunotherapeutically to activate cells of the
 CC immune system against HPV. See also AAR27723-43. (Updated on 25-MAR-2003
 CC to correct FN field.) (Updated on 24-OCT-2003 to standardise OS field)

XX SQ Sequence 271 AA;

Query Match 92.5%; Score 111; DB 2; Length 271;

Best Local Similarity 95.5%; Pred. No. 8 5e-10;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRRLRHYSVYGD 22

|||||
 Db 68 KCIDFYSRIRRLRHYSVYGD 89

RESULT 12

AAAY25385
 ID AAY25385 standard; protein; 278 AA.

XX AC AAY25385;

XX DT 06-SEP-1999 (first entry)

XX DE HPV fusion protein D1/3-E6-His/HPV18.

XX XX Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;

XX KW immunological fusion partner; CpG oligonucleotide; immune response;

XX KW HPV antigen; prevention; treatment.

XX OS Synthetic.

XX OS Human papillomavirus.

XX PN WO9933868-A2.

XX PD 08-JUL-1999.

XX PF 18-DEC-1998; 98WO-EP008563.

XX PR 24-DEC-1997; 97GB-00027262.

XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX PI Dalemans WLJ, Gerard CMG;

XX DR WPI; 1999-405485/34.

XX DR N-PSDB; AAX78800.

XX PT Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to

XX PT induce immune response to HPV.

XX PS Example XI; Page 59-60; 62pp; English.

XX CC AAX78791-X78801 represent nucleic acid sequences which encode novel
 CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
 CC HPV (represented in AAY25375-Y25386). These constructs are optionally
 CC linked to an immunological fusion partner and an immunomodulatory CpG
 CC oligonucleotide. The products of the invention can be used to induce an
 CC immune response in a patient to an HPV antigen. They can also be used for
 CC preventing or treating HPV induced tumours

XX SQ Sequence 278 AA;

Query Match 92.5%; Score 111; DB 2; Length 278;

Best Local Similarity 95.5%; Pred. No. 8.7e-10;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRRLRHYSVYGD 22

|||||
 Db 178 KCIDFYSRIRRLRHYSVYGD 199

RESULT 13

AAAY02641
 ID AAY02641 standard; protein; 278 AA.

XX AC AAY02641;

XX DT 17-OCT-2003 (revised)

XX DT 22-JUN-1999 (first entry)

XX DE Prot.D1/3-E6-His/HPV18 protein.

XX KW Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;

XX KW tumour; lesion; benign; malignant; virus; infection.

XX OS Human papillomavirus.

XX OS Haemophilus influenzae.

XX OS Chimeric.

```

PN WO9910375-A2.
XX
PD 04-MAR-1999.
XX
PF 17-AUG-1998; 98WO-EP005285.
XX
PR 22-AUG-1997; 97GB-00017953.
XX
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;
PI Lombardo-Bencheikh A;
XX WPI; 1999-190587/16.
DR N-PSDB; AAX29789.
XX
XX Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
PT treatment or prophylaxis of HPV induced lesions.
XX
XX Disclosure; Fig 22; 95pp; English.
XX
XX This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion
CC protein from Human papillomavirus (HPV) linked to an immunological fusion
CC partner, in this case, a fragment of the Haemophilus influenzae B protein
CC D. The sequence also contains a histidine tag at the C-terminus of the
CC encoded protein. The protein can be used in a vaccine, for immuno-
CC therapeutically treating HPV induced tumour lesions (benign or malignant)
CC and preventing HPV viral infection. (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
XX Sequence 278 AA;
SQ
Query Match 92.5%; Score 111; DB 2; Length 278;
Best Local Similarity 95.5%; Pred.No. 8.7e-10;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRLHYSDSVYGD 22
Db 178 KCIDFYSRIRLHYSDSVYGD 199

RESULT 14
AAY25386
ID AAY25386 standard; protein; 383 AA.
XX
AC AAY25386;
XX
XX 06-SEP-1999 (first entry)
DT
DE HPV fusion protein D1/3-E6/E7-His/HPV18.
XX
KW Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
KW immunological fusion partner; CpG oligonucleotide; immune response;
KW HPV antigen; prevention; treatment.
XX
XX Synthetic.
OS
OS Human papillomavirus.
XX
XX WO9933868-A2.
XX
XX 08-JUL-1999.
PD
XX
XX 18-DEC-1998; 98WO-EP008563.
XX
XX 24-DEC-1997; 97GB-00027262.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Dalemans WLJ, Gerard CMG;
PI
PI WPI; 1999-405485/34.
DR
DR N-PSDB; AAX78801.
XX

PT Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
PT induce immune response to HPV.
XX
XX Example XII; Page 61-62; 62pp; English.
XX
XX AAX78791-X78801 represent nucleic acid sequences which encode novel
CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
CC HPV (represented in AAY25375-Y25386). These constructs are optionally
CC linked to an immunological fusion partner and an immunomodulatory CpG
CC oligonucleotide. The products of the invention can be used to induce an
CC immune response in a patient to an HPV antigen. They can also be used for
CC preventing or treating HPV induced tumours
XX
XX Sequence 383 AA;
SQ
Query Match 92.5%; Score 111; DB 2; Length 383;
Best Local Similarity 95.5%; Pred.No. 1.2e-09;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRLHYSDSVYGD 22
Db 178 KCIDFYSRIRLHYSDSVYGD 199

RESULT 15
AAY02642
ID AAY02642 standard; protein; 383 AA.
XX
AC AAY02642;
XX
XX 17-OCT-2003 (revised)
DT
DT 22-JUN-1999 (first entry)
XX
DE Prot.D1/3-E6-E7-His/HPV18 protein.
XX
KW Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;
KW tumour; lesion; benign; malignant; virus; infection.
XX
XX Human papillomavirus.
OS
OS Haemophilus influenzae.
OS Chimeric.
XX
XX WO9910375-A2.
XX
XX 04-MAR-1999.
PD
XX
XX 17-AUG-1998; 98WO-EP005285.
PF
XX
XX 22-AUG-1997; 97GB-00017953.
PR
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;
PI Lombardo-Bencheikh A;
XX
XX WPI; 1999-190587/16.
DR N-PSDB; AAX29790.
XX
XX Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
PT treatment or prophylaxis of HPV induced lesions.
XX
XX Disclosure; Fig 25; 95pp; English.
XX
XX This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion
CC protein from Human papillomavirus (HPV) linked to an immunological fusion
CC partner, in this case, a fragment of the Haemophilus influenzae B protein
CC D. The sequence also contains a histidine tag at the C-terminus of the
CC encoded protein. The protein can be used in a vaccine, for immuno-
CC therapeutically treating HPV induced tumour lesions (benign or malignant)
CC and preventing HPV viral infection. (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
XX Sequence 383 AA;
SQ

```

Query Match 92.5%; Score 111; DB 2; Length 383;
 Best Local Similarity 95.5%; Pred No. 1.2e-09;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRIELRHYSDSVYGD 22
 |||||
 Db 178 KCIDFYSRIRIELRHYSDSVYGD 199
 |||||

Search completed: November 22, 2004, 20:27:28
 Job time : 114.5 secs

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OM protein - protein search, using sw model

Run on: November 22, 2004, 20:20:21 : Search time 27.5 Seconds
(without alignments)
53.054 Million cell updates/sec

Title: US-10-612-818-5

Perfect score: 120

Sequence: 1 KCIDFGSRIRLHRHSDSVVGD 22

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PGTUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	111	92.5	32	1	US-08-466-285-4
2	111	92.5	32	2	US-08-164-768-4
3	111	92.5	158	3	US-08-247-904B-10
4	111	92.5	158	4	US-08-767-942A-19
5	111	92.5	271	1	US-08-117-083-14
6	111	92.5	278	3	US-09-485-885-21
7	111	92.5	383	3	US-09-485-885-23
8	68	56.7	162	1	US-08-316-239B-4
9	65	54.2	158	4	US-09-980-523A-2
10	65	54.2	162	1	US-08-316-239B-3
11	65	54.2	172	3	US-08-860-165-12
12	65	54.2	172	3	US-08-860-165-14
13	65	54.2	172	3	US-09-359-382-12
14	65	54.2	172	3	US-09-359-382-14
15	65	54.2	266	3	US-08-860-165-10
16	65	54.2	266	3	US-09-359-382-10
17	65	54.2	266	4	US-09-367-309A-1
18	65	54.2	273	3	US-09-485-885-4
19	65	54.2	292	3	US-09-485-885-10
20	65	54.2	371	3	US-09-485-885-6
21	65	54.2	371	3	US-09-485-885-14
22	47	39.2	10	3	US-08-159-339A-88
23	47	39.2	20	2	US-08-934-915-44
24	47	39.2	20	2	US-08-934-915-163
25	46.5	38.8	187	3	US-08-737-248-19
26	46	38.3	347	4	US-09-248-796A-15125
27	46	38.3	1313	3	US-08-989-299-9

28	46	38.3	1313	4	US-09-407-427-9	Sequence 9, Appli
29	45.5	37.9	260	4	US-09-252-991A-23381	Sequence 23381, A
30	44	36.7	182	1	US-08-117-083-10	Sequence 10, Appl
31	43.5	36.2	365	4	US-09-134-000C-4931	Sequence 4931, Ap
32	43.5	36.2	883	4	US-09-489-039A-9716	Sequence 9716, Ap
33	43	35.8	562	4	US-09-489-039A-12840	Sequence 12840, A
34	43	35.8	1291	3	US-09-150-460B-10	Sequence 10, Appl
35	43	35.8	1291	3	US-09-220-641-5	Sequence 5, Appli
36	42	35.0	107	4	US-09-248-796A-14203	Sequence 14203, A
37	42	35.0	175	4	US-09-248-796A-20358	Sequence 20358, A
38	42	35.0	368	3	US-09-000-094-20	Sequence 20, Appl
39	42	35.0	368	4	US-10-011-749-20	Sequence 20, Appl
40	42	35.0	368	4	US-09-000-004-20	Sequence 20, Appl
41	42	35.0	375	3	US-09-000-094-22	Sequence 22, Appl
42	42	35.0	375	4	US-10-011-749-22	Sequence 22, Appl
43	42	35.0	375	4	US-09-000-004-22	Sequence 22, Appl
44	42	35.0	465	3	US-09-000-094-24	Sequence 24, Appl
45	42	35.0	465	4	US-10-011-749-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1

US-08-466-285-4

; Sequence 4, Application US/08466285

; Patent No. 5753233

; GENERAL INFORMATION:

; APPLICANT: Bieul, Conrad

; APPLICANT: Gissmann, Lutz

; APPLICANT: Muller, Martin

; TITLE OF INVENTION: Seroreactive Epitopes On Proteins Of

; TITLE OF INVENTION: Human Papillomavirus (HPV)18

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESS: Dunner

; STREET: 1300 I Street, N.W., Suite 700

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA: US/08/466,285

; APPLICATION NUMBER: US/08/466,285

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/164,768

; FILING DATE: 10-DEC-1993

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/947,992

; FILING DATE: 21-SEP-1992

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/696,953

; FILING DATE: 08-MAY-1991

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: P 40 15 044.5

; FILING DATE: 10-MAY-1990

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Manspeizer, David A.

; REGISTRATION NUMBER: 37,540

; REFERENCE/POCKET NUMBER: 05552.1075-03000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)408-4000

```

; TELEFAX: (202)408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-466-285-4

Query Match 92.5%; Score 111; DB 1; Length 32;
Best Local Similarity 95.5%; Pred. No. 2.5e-10;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRRLHYSDSVYGD 22
Db 5 KCIDFYSRIRRLHYSDSVYGD 26

RESULT 2
US-08-164-768-4
; Sequence 4, Application US/08164768
; Patent No. 6322794
; GENERAL INFORMATION:
; APPLICANT: BLEUL, Conrad
; APPLICANT: GISSMANN, Lutz
; APPLICANT: MULLER, Martin
; TITLE OF INVENTION: SEROREACTIVE EPITOPES ON PROTEINS OF
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS (HPV) 18
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
; ADDRESSEE: DUNNER, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/164,768
; FILING DATE: 10-DEC-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Forman, David S.
; REGISTRATION NUMBER: 33,694
; REFERENCE/DOCKET NUMBER: 05552.1075-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-164-768-4

Query Match 92.5%; Score 111; DB 3; Length 32;
Best Local Similarity 95.5%; Pred. No. 2.5e-10;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRRLHYSDSVYGD 22
Db 5 KCIDFYSRIRRLHYSDSVYGD 26

RESULT 3
US-08-164-768-4
; Sequence 4, Application US/08164768
; Patent No. 6322794
; GENERAL INFORMATION:
; APPLICANT: BLEUL, Conrad
; APPLICANT: GISSMANN, Lutz
; APPLICANT: MULLER, Martin
; TITLE OF INVENTION: SEROREACTIVE EPITOPES ON PROTEINS OF
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS (HPV) 18
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
; ADDRESSEE: DUNNER, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/164,768
; FILING DATE: 10-DEC-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Forman, David S.
; REGISTRATION NUMBER: 33,694
; REFERENCE/DOCKET NUMBER: 05552.1075-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-164-768-4

Query Match 92.5%; Score 111; DB 3; Length 32;
Best Local Similarity 95.5%; Pred. No. 2.5e-10;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRRLHYSDSVYGD 22
Db 5 KCIDFYSRIRRLHYSDSVYGD 26

RESULT 4
US-08-767-942A-19
; Sequence 19, Application US/08767942A
; Patent No. 6068982
; GENERAL INFORMATION:
; APPLICANT: Rolfe, Mark
; APPLICANT: Chiu, M. Isabel
; APPLICANT: Berlin, Vivian
; APPLICANT: Damagnez, Veronique
; APPLICANT: Draetta, Giulio
; APPLICANT: Guillaume, Cottarel
; TITLE OF INVENTION: UBIQUITIN CONJUGATING ENZYMES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
US-08-247-904B-10
; Sequence 10, Application US/08247904B
; Patent No. 5981699
; GENERAL INFORMATION:
; APPLICANT: Rolfe, Mark
; APPLICANT: Eckstein, Jens W.
; APPLICANT: Draetta, Giulio
; TITLE OF INVENTION: Human Ubiquitin Conjugating Enzyme
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/247,904B
; FILING DATE: 23-MAY-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-029.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-247-904B-10

Query Match 92.5%; Score 111; DB 2; Length 158;
Best Local Similarity 95.5%; Pred. No. 1.4e-09;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRRLHYSDSVYGD 22
Db 67 KCIDFYSRIRRLHYSDSVYGD 88
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,942A
; FILING DATE: 17-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-029.04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-767-942A-19

Query Match          92.5%; Score 111; DB 3; Length 158;
Best Local Similarity 95.5%; Pred. No. 1.4e-09;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRLHYSDSVYGD 22
Db 67 KCIDFYSRIRLHYSDSVYGD 88

RESULT 5
US-08-117-083-14
; Sequence 14, Application US/08117083
; Patent No. 5713054
; GENERAL INFORMATION:
; APPLICANT: Boursnell, Michael E.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..271

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; OTHER INFORMATION: /note="Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
US-08-117-083-14

Query Match          92.5%; Score 111; DB 1; Length 271;
Best Local Similarity 95.5%; Pred. No. 2.4e-09;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRLHYSDSVYGD 22
Db 68 KCIDFYSRIRLHYSDSVYGD 89

RESULT 6
US-09-485-885-21
; Sequence 21, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-21

Query Match          92.5%; Score 111; DB 3; Length 278;
Best Local Similarity 95.5%; Pred. No. 2.5e-09;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRLHYSDSVYGD 22
Db 178 KCIDFYSRIRLHYSDSVYGD 199

RESULT 7
US-09-485-885-23
; Sequence 23, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-23

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Best Local Similarity   57.1%; Pred.No. 0.018;
Matches    12; Conservative    3; Mismatches    6; Indels    0; Gaps    0;

QY      : 1 KCIDFGSRIRELRHYSDSVYG 21
         |||:|||||
Db       141 KCLFYKISEYRHVCYSLYG 161

RESULT 13
US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; FILE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match          54.2%; Score 65; DB 3; Length 172;
Best Local Similarity 57.1%; Pred.No. 0.018;
Matches    12; Conservative    3; Mismatches    6; Indels    0; Gaps    0;

QY      : 1 KCIDFGSRIRELRHYSDSVYG 21
         |||:|||||
Db       10 KCLFYKISEYRHVCYSLYG 30

RESULT 14
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; FILE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match          54.2%; Score 65; DB 3; Length 172;
Best Local Similarity 57.1%; Pred.No. 0.018;
Matches    12; Conservative    3; Mismatches    6; Indels    0; Gaps    0;

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Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRLRYHSDSVYG 21
 ||:|||||:|
 Db 141 KCLKPYSKISEYRHYCYSLYG 161

RESULT 15
 US-08-860-165-10
 ; Sequence 10, Application US/08860165A
 ; Patent No. 6004557
 ; GENERAL INFORMATION:
 ; APPLICANT: EDWARDS, Stirling John
 ; APPLICANT: COX, John Cooper
 ; APPLICANT: WEBB, Elizabeth Ann
 ; APPLICANT: FRAZER, Ian
 ; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
 ; FILE REFERENCE: 17227/130
 ; CURRENT APPLICATION NUMBER: US/08/860,165A
 ; CURRENT FILING DATE: 1997-09-22
 ; EARLIER APPLICATION NUMBER: PCT/AU95/00868
 ; EARLIER FILING DATE: 1995-12-20
 ; EARLIER APPLICATION NUMBER: AU PN0157
 ; EARLIER FILING DATE: 1994-12-20
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 266
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
 US-08-860-165-10

Query Match 54.2%; Score 65; DB 3; Length 266;
 Best Local Similarity 57.1%; Fred. NO. 0.029;
 Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRLRYHSDSVYG 21
 ||:|||||:|
 Db 72 KCLKPYSKISEYRHYCYSLYG 92

Search completed: November 22, 2004, 20:33:43
 Job time : 28.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2004, 20:19:30 ; Search time 23.5 Seconds
(without alignments)
90.075 Million cell updates/sec

Title: US-10-612-818-5
Perfect score: 120
Sequence: 1 KCIDFGSRIRRLRHYSVSDVYGD 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	111	92.5	158	1 W6WL18	E6 protein - human
2	96	80.0	158	2 S36561	E6 protein - human
3	75	62.5	158	1 W6WL39	E6 protein - human
4	71	59.2	158	1 W6WLPR	E6 protein - human
5	65	54.2	151	1 W6WL31	E6 protein - human
6	65	54.2	158	1 W6WL55	protein E6 - human
7	64	53.3	149	1 W6WL33	E6 protein - human
8	63	52.5	153	2 S36503	E6 protein - human
9	62	51.7	154	2 S36527	E6 protein - human
10	60	50.0	149	1 W6WL35	E6 protein - human
11	60	50.0	149	1 W6WL58	E6 protein - human
12	59	49.2	148	2 A51277	E6 protein - human
13	59	49.2	148	2 S36515	E6 protein - human
14	59	49.2	148	2 S36573	E6 protein - human
15	58	48.3	150	2 S36544	E6 protein - human
16	57	47.5	149	1 W6WL31	E6 protein - human
17	56	46.7	155	1 W6WL56	E6 protein - human
18	56	46.7	155	2 A44890	E6 protein - human
19	56	46.7	191	1 W6WL31	E6 protein - rhesu
20	55	45.8	153	1 S15621	E6 protein - human
21	54	45.0	150	1 W6WL42	E6 protein - human
22	54	45.0	159	1 S15614	E6 protein - human
23	54	45.0	159	2 S36497	E6 protein - human
24	51	42.5	211	2 S55129	transcription fact
25	50	41.7	142	2 S36509	E6 protein - human
26	50	41.7	410	2 T3284	hypothetical prote
27	49	40.8	936	2 T34024	hypothetical prote
28	48	40.0	155	1 W6WL43	E6 protein - human
29	47	39.2	190	2 E72748	hypothetical prote

30 47 39.2 879 2 A47704 endoglucanase I (E
31 46.5 38.6 187 2 S02304 prolactin I - chu
32 46.5 38.8 187 2 S06677 prolactin II - chu
33 46.5 38.8 210 2 S1084 prolactin precursor
34 46.5 38.8 210 2 PNO092 prolactin precursor
35 46.5 38.8 210 2 A31364 prolactin - Atlant
36 46.5 38.8 210 2 S52475 prolactin precursor
37 46.5 38.8 210 2 S34351 prolactin precursor
38 46.5 38.8 211 2 S00359 prolactin precursor
39 46 38.3 510 1 A34160 laurate omega-hydr
40 46 38.3 1313 1 J02038 peptidyl-dipeptida
41 45.5 37.9 221 1 H82999 probable hydrolase
42 45.5 37.9 1144 2 F84725 probable inositol
43 45 37.5 88 2 B69623 flagellin syntheti
44 45 37.5 182 2 E69193 conserved hypothet
45 45 37.5 509 1 O4RTLO laurate omega-hydr

ALIGNMENTS

RESULT 1
W6WL18
E6 protein - human papillomavirus type 18
C;Species: human papillomavirus type 18
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: A26165; G26251
R;Seedorf, K.; Oltersdorf, T.; Kraemer, G.; Roewekamp, W.
EMBO J. 6, 139-144, 1987
A;Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16)
A;Reference number: A91068; MUID:87218459; PMID:3034571
A;Accession: A26165
A;Molecule type: DNA
A;Residues: 1-158 <SEE>
A;Cross-references: UNIPROT:P06463; GB:X04773; NID:G60876; PIDN:CAA28466.1; PID:G60877
R;Cole, S.T.; Danos, O.
J. Mol. Biol. 193, 599-608, 1987
A;Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 18
A;Reference number: A92937; MUID:87283882; PMID:3039146
A;Accession: G26251
A;Molecule type: DNA
A;Residues: 1-158 <COL>
A;Cross-references: GB:X05015; NID:G60975; PIDN:CAA28664.1; PID:G60976
R;Matlashevski, G.; Banks, L.; Wu-Liao, J.; Spence, P.; Pin, D.; Crawford, L.
J. Gen. Virol. 67, 1909-1916, 1986
A;Title: The expression of human papillomavirus type 18 E6 protein in bacteria and the p
A;Reference number: A92791; MUID:86306665; PMID:3018129
A;Contents: annotation; identification of the protein
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;32-68/Region: zinc finger CCCC motif
F;105-141/Region: zinc finger CCCC motif

Query Match 92.5%; Score 111; DB 1; Length 158;
Best Local Similarity 95.5%; Pred. No. 1e-09;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KCIDFGSRIRRLRHYSVSDVYGD 22
DB 67 KCIDFGSRIRRLRHYSVSDVYGD 88

RESULT 2
S36561
E6 protein - human papillomavirus type 45
C;Species: human papillomavirus type 45
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36561
R;Dellus, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36561

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A:Molecule type: DNA
A:Residues: 1-158 <DEL>
A:Cross-references: UNIPROT:P21735; EMBL:X74479; NID:G397022; PIDN:CAA52573.1; PID:G3970
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match      80.0%; Score 96; DB 2; Length 158;
Best Local Similarity 81.8%; Pred. No. 2.1e-07;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 KCIDFGSRIRRLHYSDSVYGD 22
DB      67 KCIDFYSRIRLRYNSVYGE 88

RESULT 3
W6WL39
E6 protein - human papillomavirus type 39
C:Species: human papillomavirus type 39
A:Note: Host Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: A38502
R:Volpers, C.; Streeck, R.E.
Virology 181, 419-423, 1991
A:Title: Genome organization and nucleotide sequence of human papillomavirus type 39.
A:Reference number: A38502; MUID:91135017; PMID:1847266
A:Accession: A38502
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-158 <VOL>
A:Cross-references: UNIPROT:P24835; GB:M62849; EMBL:M38185; NID:G333245; PIDN:AAA47050.1
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:32-68/Region: zinc finger CCCC motif
F:105-141/Region: zinc finger CCCC motif

Query Match      62.5%; Score 75; DB 1; Length 158;
Best Local Similarity 73.7%; Pred. No. 0.00037;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      2 CIDFGSRIRRLHYSDSVY 20
DB      68 CIKFYAKIRLRYSDSVY 86

RESULT 4
W6WLPR
E6 protein - human papillomavirus type ME180 (provirus)
C:Species: human papillomavirus type ME180
A:Note: Host Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: C40509
R:Reuter, S.; Delius, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.
J. Virol. 65, 5564-5568, 1991
A:Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma
A:Reference number: A40509; MUID:91374616; PMID:1716694
A:Accession: C40509
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-158 <REU>
A:Cross-references: UNIPROT:P7962; GB:M73258
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:32-68/Region: zinc finger CCCC motif
F:105-141/Region: zinc finger CCCC motif

Query Match      59.2%; Score 71; DB 1; Length 158;
Best Local Similarity 68.4%; Pred. No. 0.0015;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      2 CIDFGSRIRRLHYSDSVY 20
DB      68 CIKFYAKIRLRYSDSVY 86

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RESULT 5
W6WL51
E6 protein - human papillomavirus type 51
C:Species: human papillomavirus type 51
A:Note: Host Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: E40415
R:Lungu, O.; Crum, C.P.; Silverstein, S.J.
J. Virol. 65, 4216-4225, 1991
A:Title: Biologic properties and nucleotide sequence analysis of human papillomavirus type
A:Reference number: A40415; MUID:91303675; PMID:1649326
A:Accession: E40415
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-151 <LUN>
A:Cross-references: UNIPROT:P26554; GB:M62877
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match      54.2%; Score 65; DB 1; Length 151;
Best Local Similarity 61.9%; Pred. No. 0.012;
Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      1 KCIDFGSRIRRLHYSDSVY 21
DB      65 QCLFYKIRLRYSDSVY 85

RESULT 6
W6WLHS
Protein E6 - human papillomavirus type 16
C:Species: human papillomavirus type 16
C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C:Accession: A03682; T10427
R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A:Title: Human papillomavirus type 16 DNA sequence.
A:Reference number: A22355; MUID:85246220; PMID:2990099
A:Accession: A03682
A:Molecule type: DNA
A:Residues: 1-158 <SEE>
A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
R:Kennedy, I.M.; Haddow, J.K.; Clements, J.S.
J. Virol. 65, 2093-2097, 1991
A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level
A:Reference number: Z17014; MUID:91162763; PMID:1848319
C:Accession: T10427
A:Status: preliminary; translated from GB/EMBL/DD5J
A:Molecule type: DNA
A:Residues: 1-158 <KEN>
A:Cross-references: EMBL:X02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
C:Genetics:
A:Gene: E6
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:37-73/Region: zinc finger CCCC motif
F:110-146/Region: zinc finger CCCC motif

Query Match      54.2%; Score 65; DB 1; Length 158;
Best Local Similarity 57.1%; Pred. No. 0.013;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      1 KCIDFGSRIRRLHYSDSVY 21
DB      72 KCLFYKIRLRYSDSVY 92

RESULT 7
W6WL33

```

E6 protein - human papillomavirus type 33
C/Species: human papillomavirus type 33
C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C/Accession: A03683
R/Cole, S.T.; Strebeck, R.E.
J. Virol. 58, 991-995, 1986

A/Title: Genome organization and nucleotide sequence of human papillomavirus type 33, wh
A/Reference number: A93020; MUID:86200464; PMID:3009902
A/Accession: A03683
A/Molecule type: DNA
A/Residues: 1-149 <COL>
A/Cross-references: UNIPROT:P06427; GB:M12732; NID:g333049; PIDN:AAA45958.1; PID:g463177
C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; zinc finger
F/30-66/Region: zinc finger CCCC motif
F/103-139/Region: zinc finger CCCC motif

Query Match 53.3%; Score 64; DB 1; Length 149;
Best Local Similarity 57.1%; Pred. No. 0.017;
Matches 12; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 CIDFGSRIRLRHYSDSYGCD 22
| : | : | : | : | : | :
Db 66 CLFLSKISRYHYNYSVGN 86

RESULT 8

S36503

E6 protein - human papillomavirus type 30
C/Species: human papillomavirus type 30
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S36503
R/Deliuss, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993

A/Description: Primer-directed sequencing of human papillomavirus types.
A/Reference number: S36469
A/Accession: S36503
A/Molecule type: DNA
A/Residues: 1-153
A/Cross-references: UNIPROT:P36809; EMBL:X74474; NID:g396973; PIDN:CAA52543.1; PID:g3969
C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 52.5%; Score 63; DB 2; Length 153;
Best Local Similarity 50.0%; Pred. No. 0.025;
Matches 10; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 2 CIDFGSRIRLRHYSDSYVG 21
| : | : | : | : | : | :
Db 69 CLLFYSKVRKIRHYNVSLEYG 88

RESULT 9

S36527

E6 protein - human papillomavirus type 53
C/Species: human papillomavirus type 53
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S36527
R/Deliuss, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993

A/Description: Primer-directed sequencing of human papillomavirus types.
A/Reference number: S36469
A/Accession: S36527
A/Molecule type: DNA
A/Residues: 1-154
A/Cross-references: UNIPROT:P36815; EMBL:X74482; NID:g397046; PIDN:CAA52591.1; PID:g3970
C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 51.7%; Score 62; DB 2; Length 154;
Best Local Similarity 55.0%; Pred. No. 0.037;
Matches 11; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Job time : 23.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 22, 2004, 20:32:01 ; Search time 97.5 Seconds
(without alignments)
79.906 Million cell updates/sec

Title: US-10-612-818-5

Perfect score: 120

Sequence: 1 KCIDFGSRIRELHYSDSVYGD 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120	100.0	22	16	US-10-612-818-5
2	111	92.5	172	16	US-10-472-724-6
3	111	92.5	278	13	US-10-000-903-21
4	111	92.5	383	13	US-10-000-903-23
5	68	56.7	151	14	US-10-177-390-6
6	65	54.2	171	16	US-10-472-724-2
7	65	54.2	266	9	US-09-367-309A-1
8	65	54.2	273	13	US-10-000-903-4
9	65	54.2	292	13	US-10-000-903-10
10	65	54.2	371	13	US-10-000-903-6
11	65	54.2	390	13	US-10-000-903-14
12	50	41.7	20	16	US-10-476-570-12
13	49	40.8	936	14	US-10-369-493-5053

14 49 40.8 961 9 US-09-220-091-3
15 48 40.0 605 16 US-10-437-963-102875
16 48 40.0 1462 15 US-10-320-797-3356
17 47 39.2 15 16 US-10-476-570-32
18 47 39.2 397 16 US-10-437-963-191497
19 46.5 38.8 187 14 US-10-140-933-39
20 46.5 38.8 187 14 US-10-140-933-41
21 46.5 38.8 187 14 US-10-140-933-40
22 46.5 38.8 189 14 US-10-140-933-42
23 46.5 38.8 794 17 US-10-425-115-275384
24 46 38.3 182 15 US-10-424-599-174143
25 46 38.3 198 15 US-10-424-599-282891
26 46 38.3 208 15 US-10-424-599-282892
27 46 38.3 324 15 US-10-424-599-282893
28 46 38.3 506 14 US-10-310-154-489
29 46 38.3 512 9 US-09-738-636-6142
30 46 38.3 890 14 US-10-389-493-3115
31 45.5 37.9 1043 15 US-10-016-248-48
32 45.5 37.9 1048 15 US-10-016-248-49
33 45.5 37.9 1274 15 US-10-467-042-11
34 45.5 37.9 1783 14 US-10-276-934-12
35 45.5 37.9 1800 14 US-10-276-934-10
36 45.5 37.9 1826 14 US-10-276-934-9
37 45.5 37.9 2306 14 US-10-276-934-11
38 45.5 37.9 2352 14 US-10-276-934-13
39 45.5 37.9 3389 15 US-10-016-248-47
40 45.5 37.9 3389 16 US-10-408-765A-2286
41 45.5 37.9 3389 15 US-10-016-248-46
42 45.5 37.9 3508 15 US-10-016-248-46
43 45 37.5 372 15 US-10-424-599-216980
44 45 37.5 509 15 US-10-074-978A-204
45 37.5 509 15 US-10-074-978A-205

ALIGNMENTS

RESULT 1
US-10-612-818-5
; Sequence 5, Application US/10612818
; Publication No. US20040110925A1
; GENERAL INFORMATION:
; APPLICANT: Impact Diagnostics
; APPLICANT: Impact Diagnostics
; TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomaviruses
; TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papillomaviruses
; TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papillomaviruses
; FILE REFERENCE: 3352-2-2
; CURRENT APPLICATION NUMBER: US/10/612,818
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 60/394,172
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 09/828,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from the E6 early coding region of HPV 18
US-10-612-818-5

Query Match 100.0%; Score 120; DB 16; Length 22;
Best Local Similarity 100.0%; Pred.No.1.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRELHYSDSVYGD 22

Db 1 KCIDFGSRIRELHYSDSVYGD 22

```

RESULT 2
US-10-472-724-6
; Sequence 6, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-6
Query Match 92.5%; Score 111; DB 16; Length 172;
Best Local Similarity 95.5%; Pred. No. 3.7e-09;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRRLRHYSDSVYGD 22
Db 73 KCIDFYSRIRRLRHYSDSVYGD 94

RESULT 3
US-10-000-903-21
; Sequence 21, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabazon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-21
Query Match 92.5%; Score 111; DB 13; Length 278;
Best Local Similarity 95.5%; Pred. No. 6.3e-09;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRRLRHYSDSVYGD 22
Db 178 KCIDFYSRIRRLRHYSDSVYGD 199

RESULT 4
US-10-000-903-23
; Sequence 23, Application US/10000903
; Publication No. US20020182221A1

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; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabazon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-23
Query Match 92.5%; Score 111; DB 13; Length 383;
Best Local Similarity 95.5%; Pred. No. 8.9e-09;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRRLRHYSDSVYGD 22
Db 178 KCIDFYSRIRRLRHYSDSVYGD 199

RESULT 5
US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505WS/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6
Query Match 56.7%; Score 68; DB 14; Length 151;
Best Local Similarity 61.9%; Pred. No. 0.016;
Matches 13; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRRLRHYSDSVYG 21
Db 65 KCLKFYSKISEYRHYCYSVYG 85

RESULT 6
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22

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; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match      54.2%; Score 65; DB 16; Length 171;
Best Local Similarity 57.1%; Pred. No. 0.054;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy      1 KCIDFGSRIRLRYHSDSVYG 21
Db      77 KCLAFYSKISEYRHYCYSLYG 97

RESULT 7
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JTM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; CURRENT APPLICATION NUMBER: US/09/367,309A
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      54.2%; Score 65; DB 9; Length 266;
Best Local Similarity 57.1%; Pred. No. 0.087;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy      1 KCIDFGSRIRLRYHSDSVYG 21
Db      72 KCLAFYSKISEYRHYCYSLYG 92

RESULT 8
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
US-10-000-903-4

Query Match      54.2%; Score 65; DB 13; Length 273;
Best Local Similarity 57.1%; Pred. No. 0.09;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy      1 KCIDFGSRIRLRYHSDSVYG 21
Db      178 KCLAFYSKISEYRHYCYSLYG 198

RESULT 9
US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
US-10-000-903-10

Query Match      54.2%; Score 65; DB 13; Length 292;
Best Local Similarity 57.1%; Pred. No. 0.096;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy      1 KCIDFGSRIRLRYHSDSVYG 21
Db      197 KCLAFYSKISEYRHYCYSLYG 217

RESULT 10
US-10-000-903-6
; Sequence 6, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
US-10-000-903-6

Query Match      54.2%; Score 65; DB 13; Length 371;
Best Local Similarity 57.1%; Pred. No. 0.096;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy      1 KCIDFGSRIRLRYHSDSVYG 21
Db      197 KCLAFYSKISEYRHYCYSLYG 217

```

```
; ORGANISM: Homo sapien
US-10-000-903-6

Query Match      54.2%; Score 65; DB 13; Length 371;
Best Local Similarity 57.1%; Pred. No. 0.13;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY   1 KCIDFGSRIRLRYHSDSVYG 21
    |||::|||::|||::|||
Db   178 KCLKPYKISBYRHYCYSLYG 198

RESULT 11
US-10-000-903-14
; Sequence 14, Application US/10000903
; Publication No. US2002018222A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bancheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-14

Query Match      54.2%; Score 65; DB 13; Length 390;
Best Local Similarity 57.1%; Pred. No. 0.13;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY   1 KCIDFGSRIRLRYHSDSVYG 21
    |||::|||::|||::|||
Db   197 KCLKPYKISBYRHYCYSLYG 217

RESULT 12
US-10-476-570-12
; Sequence 12, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 20
; TYPE: PRT
; ORGANISM: artificial sequence
US-09-220-091-3

Query Match      40.8%; Score 49; DB 9; Length 961;
Best Local Similarity 36.8%; Pred. No. 1.1e-02;
Matches 7; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY   2 CIDFGSRIRLRYHSDSVY 20
    |||::|||::|||::|||
Db   324 CTQFSGSVDARHFSDHTF 342

RESULT 14
US-09-220-091-3
; Sequence 3, Application US/09220091
; Patent No. US20020064523A1
; GENERAL INFORMATION:
; APPLICANT: H. Robert Horvitz
; APPLICANT: Xisawei Lu
; APPLICANT: Xiaowei Lu
; TITLE OF INVENTION: A TUMOR SUPPRESSOR PATHWAY IN C. ELEGANS
; FILE REFERENCE: 01997/202003
; CURRENT APPLICATION NUMBER: US/09/220,091
; CURRENT FILING DATE: 1998-12-23
; EARLIER APPLICATION NUMBER: 60/047,996
; EARLIER FILING DATE: 1997-05-28
; EARLIER APPLICATION NUMBER: 09/087,136
; EARLIER FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-220-091-3

Query Match      40.8%; Score 49; DB 9; Length 961;
Best Local Similarity 36.8%; Pred. No. 1.1e-02;
Matches 7; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
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Qy 2 CIDFGSRIRLRYSDSVY 20
 Db 349 CTQFGGSVLDARHPSDHTF 367

RESULT 15
 US-10-437-963-102875
 ; Sequence 102875, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 102875
 ; LENGTH: 605
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_100359C.1.pap
 US-10-437-963-102875

Query Match 40.0%; Score 48; DB 16; Length 605;
 Best Local Similarity 33.3%; Pred.No. 95;
 Matches 7; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 2 CIDFGSRIRLRYSDSVYGD 22
 Db 372 CVERGQRLLYVKHPSDETLD 392

Search completed: November 22, 2004, 20:48:54
 Job time : 97.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 22, 2004, 20:18:17 ; Search time 127.5 Seconds
(without alignments)
99.280 Million cell updates/sec

Title: US-10-612-818-5

Sequence: 1 KCIDFGSRIEELRHYSVYGD 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	111	92.5	158	1	VE6_HPV18
2	111	92.5	158	2	Q9NPF8
3	111	92.5	158	2	AAP20594
4	96	80.0	158	2	VE6_HPV45
5	96	80.0	158	2	Q9Y4V4
6	96	80.0	158	2	O10608
7	86	71.7	160	2	Q81984
8	82	68.3	157	2	Q9WHG0
9	81	67.5	158	1	VE6_HPV70
10	75	62.5	158	1	VE6_HPV39
11	73	60.8	151	2	Q9IR59
12	73	60.8	151	2	Q994A0
13	71	59.2	158	1	VE6_HPV68
14	71	59.2	158	1	VE6_HPVME
15	71	59.2	158	2	Q7KYX8
16	71	59.2	158	2	CAA74931
17	71	59.2	162	2	Q9UI29
18	68	56.7	84	2	Q80882
19	68	56.7	130	2	Q919B8
20	68	56.7	130	2	Q919C0
21	68	56.7	130	2	Q919C2
22	68	56.7	130	2	Q919C8
23	68	56.7	138	2	Q919D2
24	68	56.7	143	2	Q919C4
25	68	56.7	151	2	O12335
26	68	56.7	151	2	Q77J07
27	68	56.7	151	2	Q77ZJ5
28	68	56.7	151	2	Q80963
29	68	56.7	151	2	Q99648
30	68	56.7	151	2	Q89852
31	68	56.7	151	2	Q8BB19

```

32 68 56.7 151 2 Q8BB20 human papil
33 68 56.7 151 2 Q9WMP5
34 68 56.7 158 2 Q7IB17 human papil
35 68 56.7 158 2 Q9WH13 human papil
36 68 56.7 158 2 Q9QDH5 human papil
37 68 56.7 158 2 AAQ10712 human pap
38 65 54.2 90 2 Q80884
39 65 54.2 99 2 Q919B2 human papil
40 65 54.2 103 2 Q919D6
41 65 54.2 130 2 Q919B4 human papil
42 65 54.2 130 2 Q919D0
43 65 54.2 143 2 Q919B6
44 65 54.2 151 1 VE6_HPV51
45 65 54.2 151 2 O12336

```

ALIGNMENTS

```

RESULT 1
VE6_HPV18
ID_ VE6_HPV18 STANDARD; PRT; 158 AA.
AC P06463;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87283882; PubMed=3039146;
RA Cole S.P., Danos O.;
RT "Nucleotide sequence and comparative analysis of the human
RT papillomavirus type 18 genome. Phylogeny of papillomaviruses and
RT repeated structure of the E6 and E7 gene products.";
RL J. Mol. Biol. 193:599-608(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86306665; PubMed=3018129;
RA Matlashewski G., Banks L., Wu-Liao J., Spence P., Pim D., Crawford L.;
RT "The expression of human papillomavirus type 18 E6 protein in bacteria
RT and the production of anti-E6 antibodies.";
RL J. Gen. Virol. 67:1909-1916(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88188247; PubMed=2833614;
RA Inagaki Y., Tsunokawa Y., Takebe N., Nawa H., Nakanishi S., Terada M.,
RT Sugimura T.;
RT "Nucleotide sequences of cDNAs for human papillomavirus type 18
RT transcripts in HeLa cells.";
RL J. Virol. 62:1640-1646(1988).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=87053870; PubMed=3023067;
RA Schneider-Gaedcke A., Schwarz E.;
RT "Different human cervical carcinoma cell lines show similar
RT transcription patterns of human papillomavirus type 18 early genes.";
EMBO J. 5:2285-2292(1986).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=87218459; PubMed=3034571;
RA Seedorf K., Oltersdorf T., Kraemer G., Roewekamp W.;
RT "Identification of early proteins of the human papilloma viruses type
RT 16 (HPV 16) and type 18 (HPV 18) in cervical carcinoma cells.";
EMBO J. 6:139-144(1987).
RN [6]
RP ZINC-BINDING.
RX MEDLINE=89385606; PubMed=2550872;
RA Grossman S.R., Laimins L.A.;

```

RT "E6 protein of human papillomavirus type 18 binds zinc.";

OncoGene 4:1089-1093(1989).

[7]

INTERACTION WITH FBLN1, AND INHIBITION OF E6-MEDIATED TRANSFORMATION.

MEDLINE=22198366; PubMed=12200142; DOI=10.1016/S0006-291X(02)02041-7;

Du M., Fan X., Hong E., Chen J.J.;

"Interaction of oncogenic papillomavirus E6 proteins with fibulin-1.";

Biochem. Biophys. Res. Commun. 296:962-969(2002).

-!- FUNCTION: This protein has transforming activity in vitro.

-!- FUNCTION: Exhibits a strong, but non specific affinity for double

stranded DNA (in vitro).

-!- SUBUNIT: Interacts with FBLN1.

-!- SUBCELLULAR LOCATION: Nuclear matrix-associated.

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EMBL; X04354; CAA27879.1; -

EMBL; X05015; CAA28664.1; -

EMBL; M20325; AAA9514.1; -

EMBL; M26798; AAA46946.1; -

EMBL; X04773; CAA28466.1; -

EMBL; A06324; CAA00539.1; -

EMBL; A06328; CAA00542.1; -

FIR; A26165; W6WL18.

InterPro: IPR001334; E6.

Pfam: PF00518; E6; 1.

DNA-binding; Early protein; Nuclear protein; Oncogene; Zinc-finger.

ZN_FING 32 68

ZN_FING 105 141

Potential.

FT ZN_FING 22 22

CONFLICT 22 22 N -> S (in Ref. 4).

SEQUENCE 158 AA; 18871 MW; 5BCF13CF43D157FA CRC64;

Query Match 92.5%; Score 111; DB 1; Length 158;

Best Local Similarity 95.5%; Pred. No. 7e-09;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRRLRHYSVYGD 22

||||| ||||| ||||| ||||| |||||

DB 67 KCIDFYSRIRRLRHYSVYGD 88

RESULT 2

Q9QNP8 PRELIMINARY; PRT; 158 AA.

AC Q9QNP8;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE E6 protein.

OS Human papillomavirus type 18.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OC NCBI_TaxID=10582;

RN [1]

SEQUENCE FROM N.A.

RA Laasri M., Gul'ko L., Vinokurova S., Kissel'jova N., Veiko V.,

RA Kissel'jev F.;

RT "Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and

RT Transformation Potential of E7 Gene and its Mutants.";

RL Virus Genes 182:139-149(1999).

RN [2]

SEQUENCE FROM N.A.

RA Veiko V.P.;

RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

EMBL; Y18491; CAB53096.1; -

DR GO; GO:0042025; C:host cell nucleus; IEA.

DR GO; GO:0003677; F:DNA binding; IEA.

DR InterPro: IPR001334; E6.

DR Pfam: PF00518; E6; 1.

SQ SEQUENCE 158 AA; 18886 MW; 5BCF13CF43D407AF CRC64;

Query Match 92.5%; Score 111; DB 2; Length 158;

Best Local Similarity 95.5%; Pred. No. 7e-09;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRRLRHYSVYGD 22

||||| ||||| ||||| ||||| |||||

DB 67 KCIDFYSRIRRLRHYSVYGD 88

RESULT 3

AAP20594 PRELIMINARY; PRT; 158 AA.

AC AAP20594;

DT 02-MAR-2004 (TrEMBLrel. 27, Created)

DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)

DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

DE E6 protein.

OS Human papillomavirus type 18.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OC NCBI_TaxID=10582;

RN [1]

SEQUENCE FROM N.A.

RA Chen Z., Burk R.D.;

RT "The newly modified full genome sequence of HPV18 prototype (Cole,

RT 1987), with E6, E7, E1, E2, E4, E5, L2 and L1 ORFs.";

RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY262282; AAP20594.1; -

SQ SEQUENCE 158 AA; 18871 MW; 5BCF13CF43D157FA CRC64;

Query Match 92.5%; Score 111; DB 2; Length 158;

Best Local Similarity 95.5%; Pred. No. 7e-09;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRRLRHYSVYGD 22

||||| ||||| ||||| ||||| |||||

DB 67 KCIDFYSRIRRLRHYSVYGD 88

RESULT 4

VE6 HPV45 STANDARD; PRT; 158 AA.

AC P21735;

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE E6 protein.

GN Name=E6;

OS Human papillomavirus type 45.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OC NCBI_TaxID=10593;

RN [1]

SEQUENCE FROM N.A.

RA Delius H., Hofmann B.;

RT "Primer-directed sequencing of human papillomavirus types.";

RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).

RN [2]

SEQUENCE FROM N.A.

RA Kaplan J.B., Burk R.D.;

RL Submitted (AUG-1990) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: This protein has transforming activity in vitro.

CC -!- FUNCTION: Exhibits a strong, but non specific affinity for double

stranded DNA (in vitro).

CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.

CC -----

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EMBL; X74479; CAA52573.1; -	32	68	Potential.
EMBL; M38198; AAA46973.1; -	105	141	Potential.
PIR; S36561; S36561.	10	30	R -> P (in Ref. 2).
InterPro; IPR001334; B6.	30	10	I -> N (in Ref. 2).
Pfam; PF00518; B6; 1.	118	118	R -> A (in Ref. 2).
DNA-binding; Early protein; Nuclear protein; Oncogene; Zinc-finger.	158 AA;	158997 MW;	FICF10DD33AA4C3E CRC64;
FT	32	68	Potential.
FT	105	141	Potential.
FT	10	30	R -> P (in Ref. 2).
FT	30	10	I -> N (in Ref. 2).
FT	118	118	R -> A (in Ref. 2).
FT	158 AA;	158997 MW;	FICF10DD33AA4C3E CRC64;

Query Match 80.0%; Score 96; DB 1; Length 158;
Best Local Similarity 81.8%; Pred. No. 1.4e-06;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

[illegible]

RESULT 5
Q9Y4Y4
ID Q9Y4Y4
PRELIMINARY:
PRT: 158 AA.

Q24111; (T-EMBLrel. 12, Created)
01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
E6 protein. E6;
Name=HPV45 E6;
OS Homo sapiens (Human) .
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
{1}
SEQUENCE FROM N.A.
RRN
RRP
RA
RA
RRT
RRT
RRT
RRT
RRT
J. Gen. Virol. 81:198-199(2000) .
tumours.";
integration of human papillomavirus type 16 oe type 45 in two genital
"Distinct patterns of alteration of myc genes associated with
Sastre-Garau X., Favre M., Couturier J., Orth G.;

SEQUENCE FROM N.A.
Favre M.G.;
Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
EMBL; AJ242956; CAB44706.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
SEQUENCE 158 AA; 18914 MW; A61AEF98390AEBB3 CRC664;

Query Match	80.0%;	Score 96;	DB 2;	Length 158;
Best Local Similarity	81.8%;	Pred. No. 1.4e-06;		
Matches 18:	Conservative	3;	Mismatches 1;	Indels 0;
	Gaps	0;		

QY 1 KCIDFGSRIRELRHYSDSVYGD 22
 ||||| :|||:
Dp 67 KCIDFYSRIRELRYYSNSVYGE 88

RESULT 6
O10608
ID O10608
PRELIMINARY.
PRT. 158 2A

AC
010608;
01-JUL-1997 (TREMBlrel. 04, Created)

01-JUL-1997 (TReMBUrel. 04, Last sequence update)
DT
DT 01-OCT-2003 (TReMBUrel. 25, Last annotation update)
DE
DE Oncoproteins E6
OS
OS Human Papillomavirus type 45.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomaviruses.
OC NCBI_TaxID=10593;
[1] _____
RP SEQUENCE FROM N.A.
RP RA Saxtre-Garau X., Favre M., Couturier J., Orth G.;
RT "distinct patterns of alteration of myc genes associated with
RT J. Gen. Virol. 01:0-0(0).
RL
RL J. Gen. Virol. 01:0-0(0).
RL

RP SEQUENCE FROM N.A.
RA Pavre M.;
RI Submitted (MAY-1997) to the EMBL/GenBank/DBDJ databases.

DR EMBL: J15218; CAA/3660.17.
DR GO: 0042025; C: host cell nucleus; IEA.
DR GO: 0003677; F: DNA binding; IEA.
DR InterPro: IPR001334; E6.

DR Flam; PF00318; E8; L.
SQ SEQUENCE 158 AA; 18914 MW; A61AEF98390AEEB3 CRC64;
Query Match 80.0%; Score 96; DB2: Length

Best Local Similarity 81.8%; Pred. NO. 1.4E-06;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRLRYHSDSVYGD 22
 ||||| :|||:|:|:|:
 Db 67 KCIDFYSRIRLRYNSVYGE 88

RESULT 7
Q81364
TO Q81964
DDEIWINAPY.
PRT: 160 AA.

AC	Q81984;
AD	01-NOV-1996 (TrEMBLrel. 01, Created)
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	ORF putative E6 protein.

OS Human papillomavirus type 59.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.

NCBI_16610-37115;
[1]
RN
RP
SEQUENCE FROM N.A.
PY
MEDLINE=94303229; PubMed=8030272;

Choe J.; "Nucleotide sequence and phylogenetic classification of human papillomavirus type 59."; *Virology* 203:158-161(1994).

Rao J. S., Koy-Surman A., Kim H., de Villiers E.M., Matsukura I. and Kato J.; "EMBL; X77858; CAA54849.1;".

DR GO:0042025; C:host cell nucleus; IEA.

DR GO:0003677; F:DNA binding; IEA.

DR InterPro: IPR001334; E6.

DR Pfam: PF00518; E6.1.

Query Match	71.7%;	Score 86;	DB 2;	Length 160;
Best Local Similarity	68.2%;	Pred. No. 5e-05;		

QY	1	KCIDFGSRIRELRHYSDSVYGD	22
		: : : :	:
dh	67	KCTSEFARVRELRYRDSVYGE	88

RESULT 8
Q9WHG0
ID C06WHG0
PRELIMINARY.
PRT: 157 AA.


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RESULT 11
Q91R59 PRELIMINARY; PRT; 151 AA.
ID Q91R59
AC Q91R59
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 82.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=129724;
RN [1]
RP MEDLINE=20087393; PubMed=10618284;
RA Kano N., Sato T., Sato Y., Sugase M., Matsukura T.;
RT "Molecular cloning and nucleotide sequence analysis of a novel human
RT papillomavirus (Type 82) associated with vaginal intraepithelial
RT neoplasia."
RL Clin. Diagn. Lab. Immunol. 7:91-95(2000).
DR EMBL; AB027021; BAA90735.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR ZN_FING 105 141
SQ SEQUENCE 151 AA; 18006 MW; 949358742A0375B5 CRC64;

Query Match 60.8%; Score 73; DB 2; Length 151;
Best Local Similarity 71.4%; Pred. No. 0.0047;
Matches 15; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRRLRHYSVSVG 21
|||:|||||:|||||
Db 65 KCLMFYSRIRRYRSVSVG 85

RESULT 12
Q994A0 PRELIMINARY; PRT; 151 AA.
ID Q994A0
AC Q994A0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative transforming protein E6.
OS Human papillomavirus type 82.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=129724;
RN [1]
RP SEQUENCE FROM N.A.
RA Terai M., Burk R.D.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF293961; AAK28449.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR ZN_FING 105 141
SQ SEQUENCE 151 AA; 18071 MW; 55DC340E467CFFED CRC64;

Query Match 60.8%; Score 73; DB 2; Length 151;
Best Local Similarity 71.4%; Pred. No. 0.0047;
Matches 15; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRRLRHYSVSVG 21
|||:|||||:|||||
Db 65 KCLMFYSRIRRYRSVSVG 85

RESULT 13
VE6_HP68
ID VE6_HP68 STANDARD; PRT; 158 AA.
AC P54667;
DT 01-OCT-1996 (Rel. 34, Created)

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DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 68.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=45240;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97060129; PubMed=8904450;
RA Longuet M., Beaudenon S., Orth G.;
RT "Two novel genital human papillomavirus (HPV) types, HPV68 and HPV70,
RT related to the potentially oncogenic HPV39."
RL J. Clin. Microbiol. 34:738-744(1996).
CC -!- FUNCTION: Exhibits a strong, but non specific affinity for double
CC stranded DNA (in vitro).
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC
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CC
CC EMBL; X67160; CAA47632.1; -.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR DNA-binding; Early protein; Nuclear protein; Zinc-finger.
KW ZN_FING 32 68
FT ZN_FING 105 141
FT ZN_FING 105 141
SQ SEQUENCE 158 AA; 18796 MW; 46B37939CFBA6596 CRC64;

Query Match 59.2%; Score 71; DB 1; Length 158;
Best Local Similarity 68.4%; Pred. No. 0.01;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CIDFGSRIRRLRHYSVSVG 20
|||:|||||:|||||
Db 68 CIKFYAKIRRLYISVSVG 86

RESULT 14
VE6_HP68
ID VE6_HP68 STANDARD; PRT; 158 AA.
AC P27562;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type ME180.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91374616; PubMed=1716694;
RA Reuter S., Delius H., Kahn T., Hofmann B., Zur Hausen H., Schwarz E.;
RT "Characterization of a novel human papillomavirus DNA in the cervical
RT carcinoma cell line ME180."
RL J. Virol. 65:5564-5568(1991).
CC -!- FUNCTION: Exhibits a strong, but non specific affinity for double
CC stranded DNA (in vitro).
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC
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DR EMBL; W73258; -; NOT_ANNOTATED_CDS.

DR FIR; C40503; W6WLP; E6.

DR InterPro; IPR001334; E6.

DR Pfam; PF00518; E6; 1.

KW DNA-binding; Early protein; Nuclear protein; Zinc-finger.

FT ZN_FING 32 68 Potential.

FT ZN_FING 106 141 Potential.

SQ SEQUENCE 158 AA; 18738 MW; 2B1F406B563F05FC CRC64;

Query Match 59.2%; Score 71; DB 1; Length 158;

Best Local Similarity 68.4%; Pred. No. 0.01;

Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 CIDFGSRIRRLRHYSVY 20

||| :|||:||||

Db 68 CIKFKAKIRLRYSES 85

RESULT 15

Q7KYK8

ID Q7KYK8 PRELIMINARY; PRT; 158 AA.

AC Q7KYK8;

DT 05-JUL-2004 (TRENBLrel. 27, Created)

DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)

DE E6 protein.

OS Human papillomavirus type 68.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_taxid=45240;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91374616; PubMed=1716694;

RA Reuter S., Delius H., Kahn T., Hofmann B., zur Hausen H., Schwarz B.;

RT "Characterization of a novel human papillomavirus DNA in the cervical

carcinoma cell line ME180."

RL J. Virol. 65:5564-5568(1991).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=98090464; PubMed=9427755;

RA Reuter S., Bartelmann M., Vogt M., Geisen C., Napierski I., Kahn T.,

RA Delius H., Lichter P., Weitz S., Korn B., Schwarz B.;

RT "VAPM-1, a novel human gene, identified by aberrant cotranscription

with papillomavirus oncogenes in a cervical carcinoma cell line,

RT encodes a BTB/POZ-zinc finger protein with growth inhibitory

activity."

RL EMBO J. 17:215-222(1998).

DR EMBL; Y14591; CAA74931.1; -.

DR InterPro; IPR001334; E6.

DR Pfam; PF00518; E6; 1.

SQ SEQUENCE 158 AA; 18738 MW; 2B1F406B563F05FC CRC64;

Query Match 59.2%; Score 71; DB 2; Length 158;

Best Local Similarity 68.4%; Pred. No. 0.01;

Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 CIDFGSRIRRLRHYSVY 20

||| :|||:||||

Db 68 CIKFKAKIRLRYSES 85

Search completed: November 22, 2004, 20:31:49

Job time : 128.5 secs

protein seems to be valuable in the proper management of cervical cancers
for specific tumor markers.

Check Tags: Female; Human; Support, Non-U.S. Gov't

***Antibodies, Viral: AN, analysis**

Cervix Neoplasms: CH, chemistry

Cervix Neoplasms: PA, pathology

*Cervix Neoplasms: VI, virology

DNA Probes, HPV

DNA, Viral: AN, analysis

Enzyme-Linked Immunosorbent Assay

*Oncogene Proteins, Viral: AN, analysis

*Papillomavirus, Human: GE, genetics

Papillomavirus, Human: IM, immunology

Papovaviridae Infections: EP, epidemiology

Polymerase Chain Reaction

Radioimmunoassay

Seroepidemiologic Studies

*Tumor Markers, Biological: AN, analysis

0 (***Antibodies, Viral**): 0 (DNA Probes, HPV): 0 (DNA, Viral): 0 (

E6 protein, Human papillomavirus type 18): 0 (Oncogene Proteins,

Viral): 0 (Tumor Markers, Biological)

ANSWER 3 OF 11 MEDLINE on STN

1998050245 MEDLINE

Pubmed ID: 9388862

Human papillomavirus infection and esophageal squamous cell carcinoma.

He D; Tsao S W; Bu H

Department of Anatomy, Faculty of Medicine, University of Hong Kong.

Zhonghua bing li xue za zhi Chinese Journal of pathology, (1996 Dec) 25

(6) 351-4.

Journal code: 0005331. ISSN: 0529-5807.

CY China

Journal; Article; (JOURNAL ARTICLE)

LA Chinese

FS Priority Journals

EM 199801

Entered STN: 19980129

Last Updated on STN: 19980129

Entered Medline: 19980109

AB Human papillomavirus (HPV) infection, especially high risk types

HPV 16 and 18, have been studied widely in cervical

cancer. However, HPV infection in esophageal cancer has not been well

defined. In the present study, immunohistochemistry, PCR and Southern

blot hybridization methods were used to **detect** HPV infection in

127 cases of esophageal squamous cell carcinoma. Immunohistochemistry

results indicated that the virus was detected frequently in well

differentiated carcinoma. The positive rates for BPV and HPV **E6**

protein were 60.6% (77/127) and 43% (54/127) respectively. Meanwhile, PCR

and Southern hybridization showed that 35.9% (37/103) of esophageal

squamous cell carcinomas have HPV DNA, which included 20.4% (21/103)

HPV 16 and 7.8% (8/103) HPV 18. Of the 103 cases, only

I had both HPV 16 and HPV 18 DNA. Our results suggest

that HPV infection is present in esophageal squamous cell carcinoma and

may play a role in its pathogenesis.

Check Tags: Human; Male

Adult

Aged

Aged, 80 and over

***Antibodies, Viral: AN, analysis**

*Carcinoma, Squamous Cell: VI, virology

DNA, Viral: AN, analysis

English Abstract

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